



09/17/99

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Docket No. A-65686-1/RFT/RMS

Anticipated Classification of
this Application:

Class: Subclass:

Prior Application:

Examiner:

Art Unit:

"EXPRESS MAIL" MAILING LABEL

NUMBER EL451337606USDATE OF DEPOSIT September 17, 1999

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Box PATENT APPLICATION FEE
Assistant Commissioner for Patents
Washington, DC 20231

Sir:

This is a request for filing an

☐ Original☒ Continuation☐ Divisional☐ Continuation-in-part

application under 37 C.F.R. 1.53(b), in the name of Stephen D. O'Connor
(Names of ALL Applicants), for SIGNAL DETECTION TECHNIQUES FOR THE DETECTION
OF ANALYTES (Title of Invention).

1. (a) ☒ Enclosed is a new application.
(b) ☐ Enclosed is a continuation-in-part application.
(c) ☐ Enclosed is a copy of the prior application.
2. (a) ☐ Enclosed is a new Declaration.
(b) ☐ Enclosed is a copy of the prior executed Declaration as
originally filed.
(c) ☐ Enclosed is a Combined Declaration/Power of Attorney.
3. (a) ☐ Enclosed is a Small Entity Affidavit.
(b) ☐

4. ___ The filing fee is calculated below:

Claims as filed in the prior application, less any claims canceled by amendment below:

FOR:	(Col. 1) NO. FILED	(Col. 2) NO. EXTRA	SMALL ENTITY		OTHER THAN A SMALL ENTITY	
			RATE	FEE	OR RATE	FEE
BASIC FEE				\$380	OR	\$760
TOTAL CLAIMS	*** -20 =	* ***	x 9 =	\$***	OR x 18=	\$_____
INDEP CLAIMS	*** -3 =	* ***	x 39 =	\$***	OR x 78=	\$_____
[] MULTIPLE DEPENDENT CLAIM PRESENTED			+130 =	\$	OR +260=	\$_____
*If the difference in Col. 1 is less than zero, enter "0" in Col. 2.			TOTAL	\$ <u>815</u>	OR TOTAL	\$ <u>_____</u>

5. ___ The Commissioner is hereby authorized to charge any additional fees which may be required, including extension fees, or credit any overpayment to Deposit Account No. 06-1300 (Order No. A-).

6. ___ Our check in the amount of \$_____ is enclosed.

7. ___ Cancel in this application original claims _____ of the prior application before calculating the filing fee. (At least one independent claim must be retained for filing purposes.)

8. ___ Amend the specification by inserting before the first line the sentence:

--This is a X continuation ___ division ___ continuation-in-part of application Serial No. 60/100,730 filed September 17, 1999.--

9. (a) X Informal drawings are enclosed, 14 sheets.
(b) _____ Formal drawings are enclosed, _____ sheets.

10. (a) X Priority of Applications Serial No. 60/100,730 filed on September 17, 1999 in the United States of America is claimed under 35 U.S.C. 119.

(b) _____ The certified copy has been filed in prior application Serial No. _____ filed on _____.

11. ___ An Assignment is enclosed.

12. ___ The prior application is assigned of record to _____.

13. _____ A Power of Attorney by Assignee is enclosed.

14. _____ The power of attorney in the prior application is to:

(name)

(address)

(a) _____ The power appears in the original papers in the prior application.

(b) _____ Since the power does not appear in the original papers, a copy of the power in the prior application is enclosed.

(c) _____ Address all future communications to:

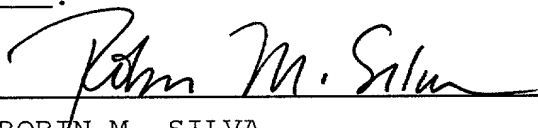
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Telephone: (415) 781-1989

15. _____ A preliminary amendment is enclosed. (Claims added by this amendment have been properly numbered consecutively beginning with the number next following the highest numbered original claim in the prior application.)

16. _____ A Prior Art Statement is enclosed.

17. _____ I hereby verify that the attached papers are a true duplicate of prior application Serial No. _____ as originally filed on _____.

Date: 9/17/99


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Registration No. 38,304

Address of Signer: _____

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Filed under Section 1.34(a)

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SIGNAL DETECTION TECHNIQUES FOR THE DETECTION OF ANALYTES

This application is a continuing application of U.S.S.N. 60/100,730, filed September 17, 1998.

FIELD OF THE INVENTION

The invention relates to the use of signal processing methods in order to achieve higher signal to noise ratios, to increase the detection limits of target analytes. These techniques include the monitoring of the output signal at higher harmonic frequencies.

BACKGROUND OF THE INVENTION

There are a number of assays and sensors for the detection of the presence and/or concentration of specific substances in fluids and gases. Many of these rely on specific ligand/antiligand reactions as the mechanism of detection. That is, pairs of substances (i.e. the binding pairs or ligand/antiligands) are known to bind to each other, while binding little or not at all to other substances. This has been the focus of a number of techniques that utilize these binding pairs for the detection of the complexes. These generally are done by labelling one component of the complex in some way, so as to make the entire complex detectable, using, for example, radioisotopes, fluorescent and other optically active molecules, enzymes, etc.

Other assays rely on electronic signals for detection. Of particular interest are biosensors. At least two types of biosensors are known; enzyme-based or metabolic biosensors and binding or bioaffinity sensors. See for example U.S. Patent No. 4,713,347; 5,192,507; 4,920,047; 3,873,267; and references disclosed therein. While some of these known sensors use alternating current (AC) techniques, these techniques are generally limited to the detection of differences in bulk (or dielectric) impedance.

Similarly, electronic detection of nucleic acids using electrodes is also known; see for example U.S. Patent Nos. 5,591,578; 5,824,473; 5,705,348; 5,780,234 and 5,770,369; U.S.S.N.s 08/873,598

08/911,589; and WO 98/20162; PCT/US98/12430; PCT/US98/12082; PCT/US99/10104; PCT/US99/01705, and PCT/US99/01703.

In the area of electrochemical sensing, there are a number of electrochemical techniques that have been employed. Traditionally, electrochemical methods generally improve their signal to noise ratios by discriminating the faradaic signal from the background components in the time domain through the application of pulsed waveforms, i.e. differential pulse polarography and square wave voltammetry. Pulse methods are able to discriminate the faradaic current from the changing current in the time domain. Changing currents decay much more rapidly than faradaic current, i.e. exponentially as compared to the inverse square root. Similarly, modulation techniques have also been used to improve signal to noise ratios; these methods utilize the imposition of a modulated carrier wave (sine wave) on the signal.

The frequency domain has only been used in a few electrochemical techniques to enhance the signal to noise ratio. In AC voltammetry, a potential ramp is applied to the electrode, and a small amplitude sine wave is superimposed on the linear ramp. However, the use of large amplitude sinusoidal voltammetry in conjunction with the detection at higher harmonic frequencies using Fourier transforms has proven to be a useful method. See U.S. Patent No. 5,650,061; Singhal et al., Anal. Chem. 69:1552 (1997); Singhal and Kuhr, Anal. Chem. 69:4828 (1997); Singhal et al., Anal. Chem. 69:3553 (1997); and Dontha et al., Anal. Chem. 69:2619 (1997), all of which are expressly incorporated by reference herein.

However, further methods are still needed to exploit signal processing advantages in detecting biomolecules such as target analytes.

Accordingly, it is an object of the invention to provide novel methods and compositions for the detection of analytes using AC techniques. These techniques find particular use in array formats, and for the detection of biomolecules such as nucleic acids and proteins.

SUMMARY OF THE INVENTION

In accordance with the objects outlined above, the present invention provides compositions and methods useful in detecting target analytes in a sample. The methods comprise providing an array comprising a plurality of electrodes, at least one of which comprises an assay complex. The assay complex comprises a capture binding ligand covalently attached to the electrode, a target analyte, and an electron transfer moiety. At least a first input signal is applied to the assay complex and an output signal is received. The output signal is then processed to detect the presence of said target analytes.

Preferred embodiments utilize a plurality of assay complexes each attached to a different cell or pad of the array.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A, 1B and 1C show actual results from DNA chips. Figure 2A plots the positives and the negatives together; Figure 2B is the positives, Figure 2C is negatives. The experiments were run as outlined in Example 1.

Figures 2A, 2B, 2C and 2D depict materials relating the use of different AC amplitudes. Figure 2A shows that when the cell is excited with a small AC amplitude, the system response is relatively linear and produces only small harmonics. Figure 2B shows that when the cell is excited with a large AC amplitude, the system response is highly nonlinear and produces only strong harmonics as observed in the frequency spectrum of the signal. Figure 2C shows the frequency spectrum and fourth harmonic AC voltammogram of a surface bound DNA system excited by $V_{ac} = 100$ mV. Figure 2D shows the response of a DNA system excited by $V_{ac} = 10$ mV at $V_{do} = 150$ mV below E_0 .

Figure 3 shows the harmonics of a square wave ACV; figure 3A is the 2d harmonic, Figure 3B is the 4th harmonic, 3C is the 6th harmonic, 3D is the 8th harmonic, 3E is the 10th harmonic, 3F is the 1,3,5 and 9th harmonics, and Figure 3G is a graph of harmonic versus current.

Figure 4 shows the results of Example 2; the frequency spectra of (A) ACV measurement of a chip with buffer solution and (B) the same chip with 1 μ M complementary DNA. The slope of the harmonic peaks is steeper in (A) compared to (B).

Figure 5 Peak amplitudes for spectra shown in Figure 4. Note the large difference in amplitude for $n \geq 2$.

Figure 6 depicts the detail of the first four peaks of the frequency spectrum for (A) a buffer measurement and (B) a 1 μ M DNA measurement.

Figure 7 show the results from the detection level study. The y-axis is the peak amplitude of the harmonics ($n \geq 2$) at different DNA concentration (1 μ M - 1 nM) and the x-axis is the frequency and harmonic number. Also shown are data from the buffer solution measurement.

Figure 8 shows a contour plot of a JTFT spectrogram using the STFT algorithm. The intensity of the contour corresponds to the amplitude of the signal. Below the spectrogram is the raw signal of the ACV scan. The frequency spectrum at the upper right hand corner is obtained from FFT.

Figure 9 shows the three-dimensional spectrogram of an ACV scan of a chip. The amplitude of the cell current is plotted on a log scale to emphasize the higher harmonics. The spectrogram clearly shows the familiar first and fourth harmonic voltammograms, without a tuned or lock-in amp. Other harmonics are also present.

Figure 10 shows the AC voltammogram response at fundamental, second, third and fourth harmonic using FFT.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is directed to the use of signal processing methods for use in the electrochemical detection of target analytes. In general, in any system, the observed signal is a combination of signal from the target analyte (sample signal) and signal from the background, or noise. For example, in AC voltammetry, two types of current are produced: faradaic current and background current. The background current can be the result of the system itself; for example, capacitive background currents are generated and can be the major component of the output signal in the systems of the invention; this is generally a product of the double layer capacitance.

The present invention is directed to the techniques that can be used to increase the signal, decrease the noise, or make the signal more obvious or detectable in a background of noise. That is, any technique that can serve to better identify a signal in the background noise may find use in the present invention. These techniques are generally classified in three ways: (1) variations in the type or methods of applying the initiation signals (i.e. varying the "input" to maximize or identify the sample signal); (2) data processing, i.e. techniques used on the "output" signals to maximize or identify the sample signal; and (3) variations in the assay itself, i.e. to the electrode surface or to the components of the system, that allow for better identification of the sample signal. Thus, for example, suitable "input" AC methods include, but are not limited to, using multiple frequencies; increasing the AC amplitude; the use of square wave ACV; the use of special or complicated waveforms; etc. Similarly, suitable "output" AC techniques include, but are not limited to, monitoring higher harmonic frequencies; phase analysis or filters; background subtraction techniques (including but not limited to impedance analysis and the use of signal recognition or peak recognition techniques); digital filtering techniques; bandwidth narrowing techniques (including lock-in detection schemes, Fast Fourier Transform (FFT) methods; correlation and/or convolution techniques; signal averaging; spectral analysis; etc.

Additionally, varying components of the assay can be done to result in the sample signal and the noise signal being altered in a non-parallel fashion; that is, the two signals respond non-linearly with respect to each other.

In general, any assay methods that rely on electrochemical detection may benefit from the techniques of the present invention. For example, the methods of the invention find use in systems that do not utilize monolayers, as well as those that do not use exogeneous ETMs and in systems that rely on techniques other than AC. However, the present invention finds particular use in systems such as are generally described in U.S. Patent Nos. 5,591,578; 5,824,473; 5,705,348; 5,780,234 and 5,770,369; U.S.S.N.s 08/873,598 08/911,589; and WO 98/20162; PCT/US98/12430; PCT/US98/12082; PCT/US99/10104; PCT/US99/01705, and PCT/US99/01703, These systems rely on the use of capture binding ligands (called capture probes when the target analyte is a nucleic acid) to anchor target analytes to the electrode surface and form an assay complex. The assay complex further comprises an electron transfer moiety (ETM), that is directly or indirectly attached to the target analyte. That is, the presence of the ETM near the electrode surface is dependent on the presence of the target analyte. Electron transfer between the ETM and the electrode is initiated using a variety of techniques as outlined below, and the output signals received and optionally processed as further outlined below. Thus, by detecting electron transfer, the presence or absence of the target analyte is determined.

In general, there are two basic detection mechanisms that may be used. In a preferred embodiment, detection of an ETM is based on electron transfer through the stacked π -orbitals of double stranded nucleic acid. This basic mechanism is described in U.S. Patent Nos. 5,591,578, 5,770,369, 5,705,348, and PCT US97/20014 and is termed "mechanism-1" herein. Briefly, previous work has shown that electron transfer can proceed rapidly through the stacked π -orbitals of double stranded nucleic acid, and significantly more slowly through single-stranded nucleic acid. Accordingly, this can serve as the basis of an assay. Thus, by adding ETMs (either covalently to one of the strands or non-covalently to the hybridization complex through the use of hybridization indicators, described below) to a nucleic acid that is attached to a detection electrode via a conductive oligomer, electron transfer between the ETM and the electrode, through the nucleic acid and conductive oligomer, may be detected.

This may be done where the target analyte is a nucleic acid; alternatively, a non-nucleic acid target analyte is used, with an optional capture binding ligand (to attach the target analyte to the detection electrode) and a soluble binding ligand that carries a nucleic acid "tail", that can then bind either directly or indirectly to a detection probe on the surface to effect detection.

Alternatively, the presence or absence of ETMs can be directly detected on a surface of a monolayer. That is, the electrons from the ETMs need not travel through the stacked π orbitals in order to generate a signal. As above, in this embodiment, the detection electrode preferably comprises a self-assembled monolayer (SAM) that serves to shield the electrode from redox-active species in the sample. In this embodiment, the presence of ETMs on the surface of a SAM, that has been formulated to comprise slight "defects" (sometimes referred to herein as "microconduits", "nanoconduits" or "electroconduits") can be directly detected. This basic idea is termed "mechanism-2" herein. Essentially, the electroconduits allow particular ETMs access to the surface. Without being bound by theory, it should be noted that the configuration of the electroconduit depends in part on the ETM chosen. For example, the use of relatively hydrophobic ETMs allows the use of hydrophobic electroconduit forming species, which effectively exclude hydrophilic or charged ETMs. Similarly, the use of more hydrophilic or charged species in the SAM may serve to exclude hydrophobic ETMs.

It should be noted that these defects are to be distinguished from "holes" that allow direct contact of sample components with the detection electrode. As is more fully outlined below, the electroconduits can be generated in several general ways, including but not limited to the use of rough electrode surfaces, such as gold electrodes formulated on PC circuit boards; or the inclusion of at least two different species in the monolayer, i.e. using a "mixed monolayer", at least one of which is a electroconduit-forming species (EFS). Thus, upon binding of a target analyte, a soluble binding ligand comprising an ETM is brought to the surface, and detection of the ETM can proceed, putatively through the "electroconduits" to the electrode. Essentially, the role of the SAM comprising the defects is to allow contact of the ETM with the electronic surface of the electrode, while still providing the benefits of shielding the electrode from solution components and reducing the amount of non-specific binding to the electrodes. Viewed differently, the role of the binding ligand is to provide specificity for a recruitment of ETMs to the surface, where they can be directly detected.

Thus, in either embodiment, as is more fully outlined below, an assay complex is formed that contains an ETM, which is then detected using the detection electrode and the signal processing techniques outlined herein.

Accordingly, the present invention provides methods of detecting a target analyte in sample solutions. As will be appreciated by those in the art, the sample solution may comprise any number of things, including, but not limited to, bodily fluids (including, but not limited to, blood, urine, serum, lymph, saliva, anal and vaginal secretions, perspiration and semen, of virtually any organism, with mammalian samples being preferred and human samples being particularly preferred); environmental samples (including, but not limited to, air, agricultural, water and soil samples); biological warfare agent samples; research samples (i.e. in the case of nucleic acids, the sample may be the products of an

amplification reaction, including both target and signal amplification as is generally described in PCT/US99/01705, such as PCR amplification reaction); purified samples, such as purified genomic DNA, RNA, proteins, etc.; raw samples (bacteria, virus, genomic DNA, etc.; As will be appreciated by those in the art, virtually any experimental manipulation may have been done on the sample.

The methods are directed to the detection of target analytes. By "target analytes" or grammatical equivalents herein is meant any molecule or compound to be detected. As outlined below, target analytes preferably bind to binding ligands, as is more fully described below. As will be appreciated by those in the art, a large number of analytes may be detected using the present methods; basically, any target analyte for which a binding ligand, described below, may be made may be detected using the methods of the invention.

Suitable analytes include organic and inorganic molecules, including biomolecules. In a preferred embodiment, the analyte may be an environmental pollutant (including pesticides, insecticides, toxins, etc.); a chemical (including solvents, organic materials, etc.); therapeutic molecules (including therapeutic and abused drugs, antibiotics, etc.); biomolecules (including hormones, cytokines, proteins, lipids, carbohydrates, cellular membrane antigens and receptors (neural, hormonal, nutrient, and cell surface receptors) or their ligands, etc); whole cells (including procaryotic (such as pathogenic bacteria) and eucaryotic cells, including mammalian tumor cells); viruses (including retroviruses, herpesviruses, adenoviruses, lentiviruses, etc.); and spores; etc. Particularly preferred analytes are environmental pollutants; nucleic acids; proteins (including enzymes, antibodies, antigens, growth factors, cytokines, etc); therapeutic and abused drugs; cells; and viruses.

Particularly preferred target analytes include proteins and nucleic acids. "Protein" as used herein includes proteins, polypeptides, and peptides. The protein may be made up of naturally occurring amino acids and peptide bonds, or synthetic peptidomimetic structures. The side chains may be in either the (R) or the (S) configuration. In the preferred embodiment, the amino acids are in the (S) or L-configuration. If non-naturally occurring side chains are used, non-amino acid substituents may be used, for example to prevent or retard in vivo degradations.

Suitable protein target analytes include, but are not limited to, (1) immunoglobulins, particularly IgEs, IgGs and IgMs, and particularly therapeutically or diagnostically relevant antibodies, including but not limited to, for example, antibodies to human albumin, apolipoproteins (including apolipoprotein E), human chorionic gonadotropin, cortisol, α -fetoprotein, thyroxine, thyroid stimulating hormone (TSH), antithrombin, antibodies to pharmaceuticals (including antiepileptic drugs (phenytoin, primidone, carbamazepine, ethosuximide, valproic acid, and phenobarbital), cardioactive drugs (digoxin, lidocaine, procainamide, and disopyramide), bronchodilators (theophylline), antibiotics (chloramphenicol,

sulfonamides), antidepressants, immunosuppressants, abused drugs (amphetamine, methamphetamine, cannabinoids, cocaine and opiates) and antibodies to any number of viruses (including orthomyxoviruses, (e.g. influenza virus), paramyxoviruses (e.g. respiratory syncytial virus, mumps virus, measles virus), adenoviruses, rhinoviruses, coronaviruses, reoviruses, togaviruses (e.g. rubella virus), parvoviruses, poxviruses (e.g. variola virus, vaccinia virus), enteroviruses (e.g. poliovirus, coxsackievirus), hepatitis viruses (including A, B and C), herpesviruses (e.g. Herpes simplex virus, varicella-zoster virus, cytomegalovirus, Epstein-Barr virus), rotaviruses, Norwalk viruses, hantavirus, arenavirus, rhabdovirus (e.g. rabies virus), retroviruses (including HIV, HTLV-I and -II), papovaviruses (e.g. papillomavirus), polyomaviruses, and picornaviruses, and the like), and bacteria (including a wide variety of pathogenic and non-pathogenic prokaryotes of interest including *Bacillus*; *Vibrio*, e.g. *V. cholerae*; *Escherichia*, e.g. Enterotoxigenic *E. coli*, *Shigella*, e.g. *S. dysenteriae*; *Salmonella*, e.g. *S. typhi*; *Mycobacterium* e.g. *M. tuberculosis*, *M. leprae*; *Clostridium*, e.g. *C. botulinum*, *C. tetani*, *C. difficile*, *C. perfringens*; *Corynebacterium*, e.g. *C. diphtheriae*; *Streptococcus*, *S. pyogenes*, *S. pneumoniae*; *Staphylococcus*, e.g. *S. aureus*; *Haemophilus*, e.g. *H. influenzae*; *Neisseria*, e.g. *N. meningitidis*, *N. gonorrhoeae*; *Yersinia*, e.g. *Y. pestis*, *Pseudomonas*, e.g. *P. aeruginosa*, *P. putida*; *Chlamydia*, e.g. *C. trachomatis*; *Bordetella*, e.g. *B. pertussis*; *Treponema*, e.g. *T. pallidum*; and the like); (2) enzymes (and other proteins), including but not limited to, enzymes used as indicators of or treatment for heart disease, including creatine kinase, lactate dehydrogenase, aspartate amino transferase, troponin T, myoglobin, fibrinogen, cholesterol, triglycerides, thrombin, tissue plasminogen activator (tPA); pancreatic disease indicators including amylase, lipase, chymotrypsin and trypsin; liver function enzymes and proteins including cholinesterase, bilirubin, and alkaline phosphatase; aldolase, prostatic acid phosphatase, terminal deoxynucleotidyl transferase, and bacterial and viral enzymes such as HIV protease; (3) hormones and cytokines (many of which serve as ligands for cellular receptors) such as erythropoietin (EPO), thrombopoietin (TPO), the interleukins (including IL-1 through IL-17), insulin, insulin-like growth factors (including IGF-1 and -2), epidermal growth factor (EGF), transforming growth factors (including TGF- α and TGF- β), human growth hormone, transferrin, epidermal growth factor (EGF), low density lipoprotein, high density lipoprotein, leptin, VEGF, PDGF, ciliary neurotrophic factor, prolactin, adrenocorticotrophic hormone (ACTH), calcitonin, human chorionic gonadotropin, cortisol, estradiol, follicle stimulating hormone (FSH), thyroid-stimulating hormone (TSH), luteinizing hormone (LH), progesterone and testosterone; and (4) other proteins (including α -fetoprotein, carcinoembryonic antigen CEA, cancer markers, etc.).

In addition, any of the biomolecules for which antibodies may be detected may be detected directly as well; that is, detection of virus or bacterial cells, therapeutic and abused drugs, etc., may be done directly.

Suitable target analytes include carbohydrates, including but not limited to, markers for breast cancer (CA15-3, CA 549, CA 27.29), mucin-like carcinoma associated antigen (MCA), ovarian cancer (CA125), pancreatic cancer (DE-PAN-2), prostate cancer (PSA), CEA, and colorectal and pancreatic cancer (CA 19, CA 50, CA242).

Suitable target analytes include metal ions, particularly heavy and/or toxic metals, including but not limited to, aluminum, arsenic, cadmium, selenium, cobalt, copper, chromium, lead, silver and nickel.

Particularly preferred target analytes are nucleic acids. In a preferred embodiment, the target analyte is a nucleic acid, and target sequences are detected. The term "target sequence" or "target nucleic acid" or grammatical equivalents herein means a nucleic acid sequence on a single strand of nucleic acid. The target sequence may be a portion of a gene, a regulatory sequence, genomic DNA, cDNA, RNA including mRNA and rRNA, or others. It may be any length, with the understanding that longer sequences are more specific. As will be appreciated by those in the art, the complementary target sequence may take many forms. For example, it may be contained within a larger nucleic acid sequence, i.e. all or part of a gene or mRNA, a restriction fragment of a plasmid or genomic DNA, among others. As is outlined more fully below, probes are made to hybridize to target sequences to determine the presence or absence of the target sequence in a sample. Generally speaking, this term will be understood by those skilled in the art. The target sequence may also be comprised of different target domains; for example, a first target domain of the sample target sequence may hybridize to a capture probe or a portion of capture extender probe, a second target domain may hybridize to a portion of an amplifier probe, a label probe, or a different capture or capture extender probe, etc. The target domains may be adjacent or separated. The terms "first" and "second" are not meant to confer an orientation of the sequences with respect to the 5'-3' orientation of the target sequence. For example, assuming a 5'-3' orientation of the complementary target sequence, the first target domain may be located either 5' to the second domain, or 3' to the second domain.

By "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, as outlined below, nucleic acid analogs are included that may have alternate backbones, comprising, for example, phosphoramidate (Beaucage et al., Tetrahedron 49(10):1925 (1993) and references therein; Letsinger, J. Org. Chem. 35:3800 (1970); Sprinzl et al., Eur. J. Biochem. 81:579 (1977); Letsinger et al., Nucl. Acids Res. 14:3487 (1986); Sawai et al, Chem. Lett. 805 (1984), Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); and Pauwels et al., Chemica Scripta 26:141 (1986)), phosphorothioate (Mag et al., Nucleic Acids Res. 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Briu et al., J. Am. Chem. Soc. 111:2321 (1989), O-methylphosphoroamidite linkages (see Eckstein, Oligonucleotides and Analogues: A Practical

Approach, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, J. Am. Chem. Soc. 114:1895 (1992); Meier et al., Chem. Int. Ed. Engl. 31:1008 (1992); Nielsen, Nature, 365:566 (1993); Carlsson et al., Nature 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., Proc. Natl. Acad. Sci. USA 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowshi et al., Angew. Chem. Intl. Ed. English 30:423 (1991); Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); Letsinger et al., Nucleoside & Nucleotide 13:1597 (1994); Chapters 2 and 3, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., Bioorganic & Medicinal Chem. Lett. 4:395 (1994); Jeffs et al., J. Biomolecular NMR 34:17 (1994); Tetrahedron Lett. 37:743 (1996)) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within the definition of nucleic acids (see Jenkins et al., Chem. Soc. Rev. (1995) pp169-176). Several nucleic acid analogs are described in Rawls, C & E News June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference. These modifications of the ribose-phosphate backbone may be done to facilitate the addition of ETMs, or to increase the stability and half-life of such molecules in physiological environments.

As will be appreciated by those in the art, all of these nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made; for example, at the site of conductive oligomer or ETM attachment, an analog structure may be used. Alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. This allows for better detection of mismatches. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The nucleic acid may be DNA, both genomic and

cDNA, RNA or a hybrid, where the nucleic acid contains any combination of deoxyribo- and ribo-nucleotides, and any combination of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. A preferred embodiment utilizes isocytosine and isoguanine in nucleic acids designed to be complementary to other probes, rather than target sequences, as this reduces non-specific hybridization, as is generally described in U.S. Patent No. 5,681,702. As used herein, the term "nucleoside" includes nucleotides as well as nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

Accordingly, in a preferred embodiment, the compositions of the invention comprise electrodes. By "electrode" herein is meant a composition, which, when connected to an electronic device, is able to sense a current or charge and convert it to a signal. Alternatively an electrode can be defined as a composition which can apply a potential to and/or pass electrons to or from species in the solution. Thus, an electrode is an ETM as described herein. Preferred electrodes are known in the art and include, but are not limited to, certain metals and their oxides, including gold; platinum; palladium; silicon; aluminum; metal oxide electrodes including platinum oxide, titanium oxide, tin oxide, indium tin oxide, palladium oxide, silicon oxide, aluminum oxide, molybdenum oxide (Mo_2O_6), tungsten oxide (WO_3) and ruthenium oxides; and carbon (including glassy carbon electrodes, graphite and carbon paste). Preferred electrodes include gold, silicon, platinum, carbon and metal oxide electrodes, with gold being particularly preferred.

The electrodes described herein are depicted as a flat surface, which is only one of the possible conformations of the electrode and is for schematic purposes only. The conformation of the electrode will vary with the detection method used. For example, flat planar electrodes may be preferred for optical detection methods, or when arrays of nucleic acids are made, thus requiring addressable locations for both synthesis and detection. Alternatively, for single probe analysis, the electrode may be in the form of a tube, with the SAMs comprising conductive oligomers and nucleic acids bound to the inner surface. Electrode coils may be preferred in some embodiments as well. This allows a maximum of surface area containing the nucleic acids to be exposed to a small volume of sample.

In a preferred embodiment, the detection electrodes are formed on a substrate. In addition, the discussion herein is generally directed to the formation of gold electrodes, but as will be appreciated by those in the art, other electrodes can be used as well. The substrate can comprise a wide variety of materials, as will be appreciated by those in the art, with printed circuit board (PCB) materials being particularly preferred. Thus, in general, the suitable substrates include, but are not limited to,

fiberglass, teflon, ceramics, glass, silicon, mica, plastic (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polycarbonate, polyurethanes, Teflon™, and derivatives thereof, etc.), GETEK (a blend of polypropylene oxide and fiberglass), etc. In some embodiments, glass may not be preferred as a substrate.

In general, preferred materials include printed circuit board materials. Circuit board materials are those that comprise an insulating substrate that is coated with a conducting layer and processed using lithography techniques, particularly photolithography techniques, to form the patterns of electrodes and interconnects (sometimes referred to in the art as interconnections or leads). The insulating substrate is generally, but not always, a polymer. As is known in the art, one or a plurality of layers may be used, to make either "two dimensional" (e.g. all electrodes and interconnections in a plane) or "three dimensional" (wherein the electrodes are on one surface and the interconnects may go through the board to the other side) boards. Three dimensional systems frequently rely on the use of drilling or etching, followed by electroplating with a metal such as copper, such that the "through board" interconnections are made. Circuit board materials are often provided with a foil already attached to the substrate, such as a copper foil, with additional copper added as needed (for example for interconnections), for example by electroplating. The copper surface may then need to be roughened, for example through etching, to allow attachment of the adhesion layer.

Accordingly, in a preferred embodiment, the present invention provides biochips (sometimes referred to herein "chips") that comprise substrates comprising a plurality of electrodes, preferably gold electrodes. The number of electrodes is as outlined for arrays. Each electrode preferably comprises a self-assembled monolayer as outlined herein. In a preferred embodiment, one of the monolayer-forming species comprises a capture ligand as outlined herein. In addition, each electrode has an interconnection, that is attached to the electrode at one end and is ultimately attached to a device that can control the electrode. That is, each electrode is independently addressable.

The substrates can be part of a larger device comprising a detection chamber that exposes a given volume of sample to the detection electrode. Generally, the detection chamber ranges from about 1 nL to 1 ml, with about 10 μ L to 500 μ L being preferred. As will be appreciated by those in the art, depending on the experimental conditions and assay, smaller or larger volumes may be used.

In some embodiments, the detection chamber and electrode are part of a cartridge that can be placed into a device comprising electronic components (an AC/DC voltage source, an ammeter, a processor, a read-out display, temperature controller, light source, etc.). In this embodiment, the interconnections from each electrode are positioned such that upon insertion of the cartridge into the device, connections between the electrodes and the electronic components are established.

Detection electrodes on circuit board material (or other substrates) are generally prepared in a wide variety of ways. In general, high purity gold is used, and it may be deposited on a surface via vacuum deposition processes (sputtering and evaporation) or solution deposition (electroplating or electroless processes). When electroplating is done, the substrate must initially comprise a conductive material; fiberglass circuit boards are frequently provided with copper foil. Frequently, depending on the substrate, an adhesion layer between the substrate and the gold in order to insure good mechanical stability is used. Thus, preferred embodiments utilize a deposition layer of an adhesion metal such as chromium, titanium, titanium/tungsten, tantalum, nickel or palladium, which can be deposited as above for the gold. When electroplated metal (either the adhesion metal or the electrode metal) is used, grain refining additives, frequently referred to in the trade as brighteners, can optionally be added to alter surface deposition properties. Preferred brighteners are mixtures of organic and inorganic species, with cobalt and nickel being preferred.

In general, the adhesion layer is from about 100 Å thick to about 25 microns (1000 microinches). The If the adhesion metal is electrochemically active, the electrode metal must be coated at a thickness that prevents “bleed-through”; if the adhesion metal is not electrochemically active, the electrode metal may be thinner. Generally, the electrode metal (preferably gold) is deposited at thicknesses ranging from about 500 Å to about 5 microns (200 microinches), with from about 30 microinches to about 50 microinches being preferred. In general, the gold is deposited to make electrodes ranging in size from about 5 microns to about 5 mm in diameter, with about 100 to 250 microns being preferred. The detection electrodes thus formed are then preferably cleaned and SAMs added, as is discussed below.

Thus, the present invention provides methods of making a substrate comprising a plurality of gold electrodes. The methods first comprise coating an adhesion metal, such as nickel or palladium (optionally with brightener), onto the substrate. Electroplating is preferred. The electrode metal, preferably gold, is then coated (again, with electroplating preferred) onto the adhesion metal. Then the patterns of the device, comprising the electrodes and their associated interconnections are made using lithographic techniques, particularly photolithographic techniques as are known in the art, and wet chemical etching. Frequently, a non-conductive chemically resistive insulating material such as solder mask or plastic is laid down using these photolithographic techniques, leaving only the electrodes and a connection point to the leads exposed; the leads themselves are generally coated.

The methods continue with the addition of SAMs. In a preferred embodiment, drop deposition techniques are used to add the required chemistry, i.e. the monolayer forming species, one of which is preferably a capture ligand comprising species. Drop deposition techniques are well known for making “spot” arrays. This is done to add a different composition to each electrode, i.e. to make an

array comprising different capture ligands. Alternatively, the SAM species may be identical for each electrode, and this may be accomplished using a drop deposition technique or the immersion of the entire substrate or a surface of the substrate into the solution.

The present system finds particular utility in array formats, i.e. wherein there is a matrix of addressable detection electrodes (herein generally referred to "pads", "addresses" or "micro-locations"). By "array" herein is meant a plurality of capture ligands in an array format; the size of the array will depend on the composition and end use of the array. Arrays containing from about 2 different capture ligands to many thousands can be made. Generally, the array will comprise from two to as many as 100,000 or more, depending on the size of the electrodes, as well as the end use of the array. Preferred ranges are from about 2 to about 10,000, with from about 5 to about 1000 being preferred, and from about 10 to about 100 being particularly preferred. In some embodiments, the compositions of the invention may not be in array format; that is, for some embodiments, compositions comprising a single capture ligand may be made as well. In addition, in some arrays, multiple substrates may be used, either of different or identical compositions. Thus for example, large arrays may comprise a plurality of smaller substrates.

In a preferred embodiment, although in many systems this is not required, the electrode comprises a self-assembled monolayer (SAM). As outlined herein, the efficiency of target analyte binding (for example, oligonucleotide hybridization) may increase when the analyte is at a distance from the electrode. Similarly, non-specific binding of biomolecules, including the target analytes, to an electrode is generally reduced when a monolayer is present. Thus, a monolayer facilitates the maintenance of the analyte away from the electrode surface. In addition, a monolayer serves to keep charged species away from the surface of the electrode. Thus, this layer helps to prevent electrical contact between the electrodes and the ETMs, or between the electrode and charged species within the solvent. Such contact can result in a direct "short circuit" or an indirect short circuit via charged species which may be present in the sample. Accordingly, the monolayer is preferably tightly packed in a uniform layer on the electrode surface, such that a minimum of "holes" exist. The monolayer thus serves as a physical barrier to block solvent accessibility to the electrode.

By "monolayer" or "self-assembled monolayer" or "SAM" herein is meant a relatively ordered assembly of molecules spontaneously chemisorbed on a surface, in which the molecules are oriented approximately parallel to each other and roughly perpendicular to the surface. Each of the molecules includes a functional group that adheres to the surface, and a portion that interacts with neighboring molecules in the monolayer to form the relatively ordered array. A "mixed" monolayer comprises a heterogeneous monolayer, that is, where at least two different molecules make up the monolayer.

In general, the SAMs of the invention can be generated in a number of ways and comprise a number of different components, depending on the electrode surface and the system used. For “mechanism-1” embodiments, preferred embodiments utilize two monolayer forming species: a monolayer forming species (including insulators or conductive oligomers) and a conductive oligomer species comprising the capture binding ligand, although as will be appreciated by those in the art, additional monolayer forming species can be included as well. For “mechanism-2” systems, the composition of the SAM depends on the detection electrode surface. In general, two basic “mechanism-2” systems are described; detection electrodes comprising “smooth” surfaces, such as gold ball electrodes, and those comprising “rough” surfaces, such as those that are made using commercial processes on PC circuit boards. In general, without being bound by theory, it appears that monolayers made on imperfect surfaces, i.e. “rough” surfaces, spontaneously form monolayers containing enough electroconduits even in the absence of electroconduit-forming species (EFS), probably due to the fact that the formation of a uniform monolayer on a rough surface is difficult. “Smoother” surfaces, however, may require the inclusion of sufficient numbers of EFS to generate the electroconduits, as the uniform surfaces allow a more uniform monolayer to form. Again, without being bound by theory, the inclusion of species that disturb the uniformity of the monolayer, for example by including a rigid molecule in a background of more flexible ones, causes electroconduits. Thus “smooth” surfaces comprise monolayers comprising three components: an insulator species, a EFS, and a species comprising the capture ligand, although in some circumstances, for example when the capture ligand species is included at high density, the capture ligand species can serve as the EFS. “Smoothness” in this context is not measured physically but rather as a function of an increase in the measured signal when EFS are included. That is, the signal from a detection electrode coated with monolayer forming species is compared to a signal from a detection electrode coated with monolayer forming species including a EFS. An increase indicates that the surface is relatively smooth, since the inclusion of a EFS served to facilitate the access of the ETM to the electrode. It should also be noted that while the discussion herein is mainly directed to gold electrodes and thiol-containing monolayer forming species, other types of electrodes and monolayer-forming species can be used.

It should be noted that the “electroconduits” of mechanism-2 systems do not result in direct contact of sample components with the electrode surface; that is, the electroconduits are not large pores or holes that allow physical access to the electrode. Rather, without being bound by theory, it appears that the electroconduits allow certain types of ETMs, particularly hydrophobic ETMs, to penetrate sufficiently into the monolayer to allow detection. However, other types of redox active species, including some hydrophilic species, do not penetrate into the monolayer, even with electroconduits present. Thus, in general, redox active species that may be present in the sample do not give substantial signals as a result of the electroconduits. While the exact system will vary with the composition of the SAM and the choice of the ETM, in general, the test for a suitable SAM to reduce non-specific binding that also has

sufficient electroconduits for ETM detection is to add either ferrocene or ferrocyanide to the SAM; the former should give a signal and the latter should not.

Accordingly, in mechanism-1 systems, the monolayer comprises a first species comprising a conductive oligomer comprising the capture binding ligand, as is more fully outlined below, and a second species comprising a monolayer forming species, including either or both insulators or conductive oligomers.

In a preferred embodiment, the monolayer comprises electroconduit-forming species. By “electroconduit-forming species” or “EFS” herein is meant a molecule that is capable of generating sufficient electroconduits in a monolayer, generally of insulators such as alkyl groups, to allow detection of ETMs at the surface. In general, EFS have one or more of the following qualities: they may be relatively rigid molecules, for example as compared to an alkyl chain; they may attach to the electrode surface with a geometry different from the other monolayer forming species (for example, alkyl chains attached to gold surfaces with thiol groups are thought to attach at roughly 45° angles, and phenyl-acetylene chains attached to gold via thiols are thought to go down at 90° angles); they may have a structure that sterically interferes or interrupts the formation of a tightly packed monolayer, for example through the inclusion of branching groups such as alkyl groups, or the inclusion of highly flexible species, such as polyethylene glycol units; or they may be capable of being activated to form electroconduits; for example, photoactivatable species that can be selectively removed from the surface upon photoactivation, leaving electroconduits.

Preferred EFS include conductive oligomers, as defined below, and phenyl-acetylene-polyethylene glycol species. However, in some embodiments, the EFS is not a conductive oligomer.

In a preferred embodiment, the monolayer comprises conductive oligomers. By “conductive oligomer” herein is meant a substantially conducting oligomer, preferably linear, some embodiments of which are referred to in the literature as “molecular wires”. By “substantially conducting” herein is meant that the oligomer is capable of transferring electrons at 100 Hz. Generally, the conductive oligomer has substantially overlapping π -orbitals, i.e. conjugated π -orbitals, as between the monomeric units of the conductive oligomer, although the conductive oligomer may also contain one or more sigma (σ) bonds. Additionally, a conductive oligomer may be defined functionally by its ability to inject or receive electrons into or from an associated ETM. Furthermore, the conductive oligomer is more conductive than the insulators as defined herein. Additionally, the conductive oligomers of the invention are to be distinguished from electroactive polymers, that themselves may donate or accept electrons.

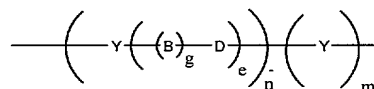
In a preferred embodiment, the conductive oligomers have a conductivity, S , of from between about 10^{-6} to about $10^4 \Omega^{-1}\text{cm}^{-1}$, with from about 10^{-5} to about $10^3 \Omega^{-1}\text{cm}^{-1}$ being preferred, with these S values being calculated for molecules ranging from about 20\AA to about 200\AA . As described below, insulators have a conductivity S of about $10^{-7} \Omega^{-1}\text{cm}^{-1}$ or lower, with less than about $10^{-8} \Omega^{-1}\text{cm}^{-1}$ being preferred. See generally Gardner et al., *Sensors and Actuators A* 51 (1995) 57-66, incorporated herein by reference.

Desired characteristics of a conductive oligomer include high conductivity, sufficient solubility in organic solvents and/or water for synthesis and use of the compositions of the invention, and preferably chemical resistance to reactions that occur i) during binding ligand synthesis (i.e. nucleic acid synthesis, such that nucleosides containing the conductive oligomers may be added to a nucleic acid synthesizer during the synthesis of the compositions of the invention, ii) during the attachment of the conductive oligomer to an electrode, or iii) during binding assays. In addition, conductive oligomers that will promote the formation of self-assembled monolayers are preferred.

The oligomers of the invention comprise at least two monomeric subunits, as described herein. As is described more fully below, oligomers include homo- and hetero-oligomers, and include polymers.

In a preferred embodiment, the conductive oligomer has the structure depicted in Structure 1:

Structure 1



As will be understood by those in the art, all of the structures depicted herein may have additional atoms or structures; i.e. the conductive oligomer of Structure 1 may be attached to ETMs, such as electrodes, transition metal complexes, organic ETMs, and metallocenes, and to binding ligands such as nucleic acids, or to several of these. Unless otherwise noted, the conductive oligomers depicted herein will be attached at the left side to an electrode; that is, as depicted in Structure 1, the left "Y" is connected to the electrode as described herein. If the conductive oligomer is to be attached to a binding ligand, the right "Y", if present, is attached to the binding ligand such as a nucleic acid, either directly or through the use of a linker, as is described herein.

In this embodiment, Y is an aromatic group, n is an integer from 1 to 50, g is either 1 or zero, e is an integer from zero to 10, and m is zero or 1. When g is 1, B-D is a bond able to conjugate with neighboring bonds (herein referred to as a Conjugated bond@), preferably selected from acetylene, alkene, substituted alkene, amide, azo, -C=N- (including -N=C-, -CR=N- and -N=CR-), -Si=Si-, and -Si=C- (including -C=Si-, -Si=CR- and -CR=Si-). When g is zero, e is preferably 1, D is preferably

carbonyl, or a heteroatom moiety, wherein the heteroatom is selected from oxygen, sulfur, nitrogen, silicon or phosphorus. Thus, suitable heteroatom moieties include, but are not limited to, -NH and -NR, wherein R is as defined herein; substituted sulfur; sulfonyl (-SO₂-) sulfoxide (-SO-); phosphine oxide (-PO- and -RPO-); and thiophosphine (-PS- and -RPS-). However, when the conductive oligomer is to be attached to a gold electrode, as outlined below, sulfur derivatives are not preferred.

By "aromatic group" or grammatical equivalents herein is meant an aromatic monocyclic or polycyclic hydrocarbon moiety generally containing 5 to 14 carbon atoms (although larger polycyclic rings structures may be made) and any carbocyclic ketone or thioketone derivative thereof, wherein the carbon atom with the free valence is a member of an aromatic ring. Aromatic groups include arylene groups and aromatic groups with more than two atoms removed. For the purposes of this application aromatic includes heterocycle. "Heterocycle" or "heteroaryl" means an aromatic group wherein 1 to 5 of the indicated carbon atoms are replaced by a heteroatom chosen from nitrogen, oxygen, sulfur, phosphorus, boron and silicon wherein the atom with the free valence is a member of an aromatic ring, and any heterocyclic ketone and thioketone derivative thereof. Thus, heterocycle includes thienyl, furyl, pyrrolyl, pyrimidinyl, oxalyl, indolyl, purinyl, quinolyl, isoquinolyl, thiazolyl, imidozyl, etc.

Importantly, the Y aromatic groups of the conductive oligomer may be different, i.e. the conductive oligomer may be a heterooligomer. That is, a conductive oligomer may comprise a oligomer of a single type of Y groups, or of multiple types of Y groups.

The aromatic group may be substituted with a substitution group, generally depicted herein as R. R groups may be added as necessary to affect the packing of the conductive oligomers, i.e. R groups may be used to alter the association of the oligomers in the monolayer. R groups may also be added to 1) alter the solubility of the oligomer or of compositions containing the oligomers; 2) alter the conjugation or electrochemical potential of the system; and 3) alter the charge or characteristics at the surface of the monolayer.

In a preferred embodiment, when the conductive oligomer is greater than three subunits, R groups are preferred to increase solubility when solution synthesis is done. However, the R groups, and their positions, are chosen to minimally effect the packing of the conductive oligomers on a surface, particularly within a monolayer, as described below. In general, only small R groups are used within the monolayer, with larger R groups generally above the surface of the monolayer. Thus for example the attachment of methyl groups to the portion of the conductive oligomer within the monolayer to increase solubility is preferred, with attachment of longer alkoxy groups, for example, C3 to C10, is preferably done above the monolayer surface. In general, for the systems described herein, this

generally means that attachment of sterically significant R groups is not done on any of the first two or three oligomer subunits, depending on the average length of the molecules making up the monolayer.

Suitable R groups include, but are not limited to, hydrogen, alkyl, alcohol, aromatic, amino, amido, nitro, ethers, esters, aldehydes, sulfonyl, silicon moieties, halogens, sulfur containing moieties, phosphorus containing moieties, and ethylene glycols. In the structures depicted herein, R is hydrogen when the position is unsubstituted. It should be noted that some positions may allow two substitution groups, R and R', in which case the R and R' groups may be either the same or different.

By "alkyl group" or grammatical equivalents herein is meant a straight or branched chain alkyl group, with straight chain alkyl groups being preferred. If branched, it may be branched at one or more positions, and unless specified, at any position. The alkyl group may range from about 1 to about 30 carbon atoms (C1 -C30), with a preferred embodiment utilizing from about 1 to about 20 carbon atoms (C1 -C20), with about C1 through about C12 to about C15 being preferred, and C1 to C5 being particularly preferred, although in some embodiments the alkyl group may be much larger. Also included within the definition of an alkyl group are cycloalkyl groups such as C5 and C6 rings, and heterocyclic rings with nitrogen, oxygen, sulfur or phosphorus. Alkyl also includes heteroalkyl, with heteroatoms of sulfur, oxygen, nitrogen, and silicone being preferred. Alkyl includes substituted alkyl groups. By "substituted alkyl group" herein is meant an alkyl group further comprising one or more substitution moieties "R", as defined above.

By "amino groups" or grammatical equivalents herein is meant -NH₂, -NHR and -NR₂ groups, with R being as defined herein.

By "nitro group" herein is meant an -NO₂ group.

By "sulfur containing moieties" herein is meant compounds containing sulfur atoms, including but not limited to, thia-, thio- and sulfo- compounds, thiols (-SH and -SR), and sulfides (-RSR-). By "phosphorus containing moieties" herein is meant compounds containing phosphorus, including, but not limited to, phosphines and phosphates. By "silicon containing moieties" herein is meant compounds containing silicon.

By "ether" herein is meant an -O-R group. Preferred ethers include alkoxy groups, with -O-(CH₂)₂CH₃ and -O-(CH₂)₄CH₃ being preferred.

By "ester" herein is meant a -COOR group.

By "halogen" herein is meant bromine, iodine, chlorine, or fluorine. Preferred substituted alkyls are partially or fully halogenated alkyls such as CF_3 , etc.

By "aldehyde" herein is meant -RCHO groups.

By "alcohol" herein is meant -OH groups, and alkyl alcohols -ROH .

By "amido" herein is meant -RCONH- or RCONR- groups.

By "ethylene glycol" or "(poly)ethylene glycol" herein is meant a $\text{-(O-CH}_2\text{-CH}_2\text{)}_n\text{-}$ group, although each carbon atom of the ethylene group may also be singly or doubly substituted, i.e. $\text{-(O-CR}_2\text{-CR}_2\text{)}_n\text{-}$, with R as described above. Ethylene glycol derivatives with other heteroatoms in place of oxygen (i.e. $\text{-(N-CH}_2\text{-CH}_2\text{)}_n\text{-}$ or $\text{-(S-CH}_2\text{-CH}_2\text{)}_n\text{-}$, or with substitution groups) are also preferred.

Preferred substitution groups include, but are not limited to, methyl, ethyl, propyl, alkoxy groups such as $\text{-O-(CH}_2\text{)}_2\text{CH}_3$ and $\text{-O-(CH}_2\text{)}_4\text{CH}_3$ and ethylene glycol and derivatives thereof.

Preferred aromatic groups include, but are not limited to, phenyl, naphthyl, naphthalene, anthracene, phenanthroline, pyrrole, pyridine, thiophene, porphyrins, and substituted derivatives of each of these, included fused ring derivatives.

In the conductive oligomers depicted herein, when g is 1, B-D is a bond linking two atoms or chemical moieties. In a preferred embodiment, B-D is a conjugated bond, containing overlapping or conjugated π -orbitals.

Preferred B-D bonds are selected from acetylene ($\text{-C}\equiv\text{C-}$, also called alkyne or ethyne), alkene (-CH=CH- , also called ethylene), substituted alkene (-CR=CR- , -CH=CR- and -CR=CH-), amide (-NH-CO- and -NR-CO- or -CO-NH- and -CO-NR-), azo (-N=N-), esters and thioesters (-CO-O- , -O-CO- , -CS-O- and -O-CS-) and other conjugated bonds such as (-CH=N- , -CR=N- , -N=CH- and -N=CR-), (-SiH=SiH- , -SiR=SiH- , -SiR=SiH- , and -SiR=SiR-), (-SiH=CH- , -SiR=CH- , -SiH=CR- , -SiR=CR- , -CH=SiH- , -CR=SiH- , -CH=SiR- , and -CR=SiR-). Particularly preferred B-D bonds are acetylene, alkene, amide, and substituted derivatives of these three, and azo. Especially preferred B-D bonds are acetylene, alkene and amide. The oligomer components attached to double bonds may be in the trans or cis conformation, or mixtures. Thus, either B or D may include carbon, nitrogen or silicon. The substitution groups are as defined as above for R.

When $g=0$ in the Structure 1 conductive oligomer, e is preferably 1 and the D moiety may be carbonyl or a heteroatom moiety as defined above.

As above for the Y rings, within any single conductive oligomer, the B-D bonds (or D moieties, when $g=0$) may be all the same, or at least one may be different. For example, when m is zero, the terminal B-D bond may be an amide bond, and the rest of the B-D bonds may be acetylene bonds. Generally, when amide bonds are present, as few amide bonds as possible are preferable, but in some embodiments all the B-D bonds are amide bonds. Thus, as outlined above for the Y rings, one type of B-D bond may be present in the conductive oligomer within a monolayer as described below, and another type above the monolayer level, for example to give greater flexibility for nucleic acid hybridization when the nucleic acid is attached via a conductive oligomer.

In the structures depicted herein, n is an integer from 1 to 50, although longer oligomers may also be used (see for example Schumm et al., *Angew. Chem. Int. Ed. Engl.* 1994 33(13):1360). Without being bound by theory, it appears that for efficient hybridization of nucleic acids on a surface, the hybridization should occur at a distance from the surface, i.e. the kinetics of hybridization increase as a function of the distance from the surface, particularly for long oligonucleotides of 200 to 300 basepairs. Accordingly, when a nucleic acid is attached via a conductive oligomer, as is more fully described below, the length of the conductive oligomer is such that the closest nucleotide of the nucleic acid is positioned from about 6Å to about 100Å (although distances of up to 500Å may be used) from the electrode surface, with from about 15Å to about 60Å being preferred and from about 25Å to about 60Å also being preferred. Accordingly, n will depend on the size of the aromatic group, but generally will be from about 1 to about 20, with from about 2 to about 15 being preferred and from about 3 to about 10 being especially preferred.

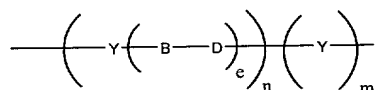
In the structures depicted herein, m is either 0 or 1. That is, when m is 0, the conductive oligomer may terminate in the B-D bond or D moiety, i.e. the D atom is attached to the nucleic acid either directly or via a linker. In some embodiments, for example when the conductive oligomer is attached to a phosphate of the ribose-phosphate backbone of a nucleic acid, there may be additional atoms, such as a linker, attached between the conductive oligomer and the nucleic acid. Additionally, as outlined below, the D atom may be the nitrogen atom of the amino-modified ribose. Alternatively, when m is 1, the conductive oligomer may terminate in Y, an aromatic group, i.e. the aromatic group is attached to the nucleic acid or linker.

As will be appreciated by those in the art, a large number of possible conductive oligomers may be utilized. These include conductive oligomers falling within the Structure 1 and Structure 8 formulas, as well as other conductive oligomers, as are generally known in the art, including for example,

compounds comprising fused aromatic rings or Teflon®-like oligomers, such as $-(CF_2)_n-$, $-(CHF)_n-$ and $-(CFR)_n-$. See for example, Schumm et al., *Angew. Chem. Intl. Ed. Engl.* 33:1361 (1994); Grosshenny et al., *Platinum Metals Rev.* 40(1):26-35 (1996); Tour, *Chem. Rev.* 96:537-553 (1996); Hsung et al., *Organometallics* 14:4808-4815 (1995; and references cited therein, all of which are expressly incorporated by reference.

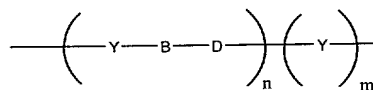
Particularly preferred conductive oligomers of this embodiment are depicted below:

Structure 2



Structure 2 is Structure 1 when g is 1. Preferred embodiments of Structure 2 include: e is zero, Y is pyrrole or substituted pyrrole; e is zero, Y is thiophene or substituted thiophene; e is zero, Y is furan or substituted furan; e is zero, Y is phenyl or substituted phenyl; e is zero, Y is pyridine or substituted pyridine; e is 1, B-D is acetylene and Y is phenyl or substituted phenyl (see Structure 4 below). A preferred embodiment of Structure 2 is also when e is one, depicted as Structure 3 below:

Structure 3

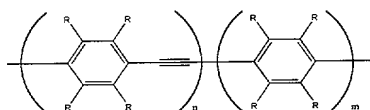


Preferred embodiments of Structure 3 are: Y is phenyl or substituted phenyl and B-D is azo; Y is phenyl or substituted phenyl and B-D is acetylene; Y is phenyl or substituted phenyl and B-D is alkene; Y is pyridine or substituted pyridine and B-D is acetylene; Y is thiophene or substituted thiophene and B-D is acetylene; Y is furan or substituted furan and B-D is acetylene; Y is thiophene or furan (or substituted thiophene or furan) and B-D are alternating alkene and acetylene bonds.

Most of the structures depicted herein utilize a Structure 3 conductive oligomer. However, any Structure 3 oligomers may be substituted with any of the other structures depicted herein, i.e. Structure 1 or 8 oligomer, or other conducting oligomer, and the use of such Structure 3 depiction is not meant to limit the scope of the invention.

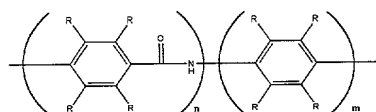
Particularly preferred embodiments of Structure 3 include Structures 4, 5, 6 and 7, depicted below:

Structure 4



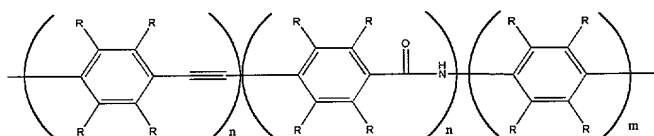
Particularly preferred embodiments of Structure 4 include: n is two, m is one, and R is hydrogen; n is three, m is zero, and R is hydrogen; and the use of R groups to increase solubility.

Structure 5



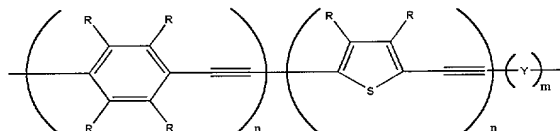
When the B-D bond is an amide bond, as in Structure 5, the conductive oligomers are pseudopeptide oligomers. Although the amide bond in Structure 5 is depicted with the carbonyl to the left, i.e. -CONH-, the reverse may also be used, i.e. -NHCO-. Particularly preferred embodiments of Structure 5 include: n is two, m is one, and R is hydrogen; n is three, m is zero, and R is hydrogen (in this embodiment, the terminal nitrogen (the D atom) may be the nitrogen of the amino-modified ribose); and the use of R groups to increase solubility.

Structure 6



Preferred embodiments of Structure 6 include the first n is two, second n is one, m is zero, and all R groups are hydrogen, or the use of R groups to increase solubility.

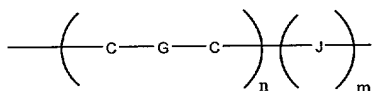
Structure 7



Preferred embodiments of Structure 7 include: the first n is three, the second n is from 1-3, with m being either 0 or 1, and the use of R groups to increase solubility.

In a preferred embodiment, the conductive oligomer has the structure depicted in Structure 8:

Structure 8



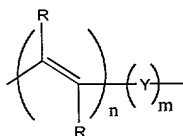
In this embodiment, C are carbon atoms, n is an integer from 1 to 50, m is 0 or 1, J is a heteroatom selected from the group consisting of oxygen, nitrogen, silicon, phosphorus, sulfur, carbonyl or sulfoxide, and G is a bond selected from alkane, alkene or acetylene, such that together with the two carbon atoms the C-G-C group is an alkene (-CH=CH-), substituted alkene (-CR=CR-) or mixtures thereof (-CH=CR- or -CR=CH-), acetylene (-C≡C-), or alkane (-CR₂-CR₂-, with R being either

hydrogen or a substitution group as described herein). The G bond of each subunit may be the same or different than the G bonds of other subunits; that is, alternating oligomers of alkene and acetylene bonds could be used, etc. However, when G is an alkane bond, the number of alkane bonds in the oligomer should be kept to a minimum, with about six or less sigma bonds per conductive oligomer being preferred. Alkene bonds are preferred, and are generally depicted herein, although alkane and acetylene bonds may be substituted in any structure or embodiment described herein as will be appreciated by those in the art.

In some embodiments, for example when ETMs are not present, if $m=0$ then at least one of the G bonds is not an alkane bond.

In a preferred embodiment, the m of Structure 8 is zero. In a particularly preferred embodiment, m is zero and G is an alkene bond, as is depicted in Structure 9:

Structure 9



The alkene oligomer of structure 9, and others depicted herein, are generally depicted in the preferred trans configuration, although oligomers of cis or mixtures of trans and cis may also be used. As above, R groups may be added to alter the packing of the compositions on an electrode, the hydrophilicity or hydrophobicity of the oligomer, and the flexibility, i.e. the rotational, torsional or longitudinal flexibility of the oligomer. n is as defined above.

In a preferred embodiment, R is hydrogen, although R may be also alkyl groups and polyethylene glycols or derivatives.

In an alternative embodiment, the conductive oligomer may be a mixture of different types of oligomers, for example of structures 1 and 8.

The conductive oligomers may or may not have terminal groups. Thus, in a preferred embodiment, there is no additional terminal group, and the conductive oligomer terminates with one of the groups depicted in Structures 1 to 9; for example, a B-D bond such as an acetylene bond. Alternatively, in a preferred embodiment, a terminal group is added, sometimes depicted herein as "Q". A terminal group may be used for several reasons; for example, to contribute to the electronic availability of the conductive oligomer for detection of ETMs, or to alter the surface of the SAM for other reasons, for example to prevent non-specific binding. For example, when the target analyte is a nucleic acid, there

may be negatively charged groups on the terminus to form a negatively charged surface such that when the nucleic acid is DNA or RNA the nucleic acid is repelled or prevented from lying down on the surface, to facilitate hybridization. Preferred terminal groups include -NH_2 , -OH , -COOH , and alkyl groups such as -CH_3 , and (poly)alkyloxides such as (poly)ethylene glycol, with $\text{-OCH}_2\text{CH}_2\text{OH}$, $\text{-(OCH}_2\text{CH}_2\text{O)}_2\text{H}$, $\text{-(OCH}_2\text{CH}_2\text{O)}_3\text{H}$, and $\text{-(OCH}_2\text{CH}_2\text{O)}_4\text{H}$ being preferred.

In one embodiment, it is possible to use mixtures of conductive oligomers with different types of terminal groups. Thus, for example, some of the terminal groups may facilitate detection, and some may prevent non-specific binding.

It will be appreciated that the monolayer may comprise different conductive oligomer species, although preferably the different species are chosen such that a reasonably uniform SAM can be formed. Thus, for example, when capture binding ligands such as nucleic acids are covalently attached to the electrode using conductive oligomers, it is possible to have one type of conductive oligomer used to attach the nucleic acid, and another type in the SAM. Similarly, it may be desirable to have mixtures of different lengths of conductive oligomers in the monolayer, to help reduce non-specific signals. Thus, for example, preferred embodiments utilize conductive oligomers that terminate below the surface of the rest of the monolayer, i.e. below the insulator layer, if used, or below some fraction of the other conductive oligomers. Similarly, the use of different conductive oligomers may be done to facilitate monolayer formation, or to make monolayers with altered properties.

In a preferred embodiment, the monolayer may further comprise insulator moieties. By "insulator" herein is meant a substantially nonconducting oligomer, preferably linear. By "substantially nonconducting" herein is meant that the insulator will not transfer electrons at 100 Hz. The rate of electron transfer through the insulator is preferably slower than the rate through the conductive oligomers described herein.

In a preferred embodiment, the insulators have a conductivity, S , of about $10^{-7} \Omega^{-1}\text{cm}^{-1}$ or lower, with less than about $10^{-8} \Omega^{-1}\text{cm}^{-1}$ being preferred. See generally Gardner et al., supra.

Generally, insulators are alkyl or heteroalkyl oligomers or moieties with sigma bonds, although any particular insulator molecule may contain aromatic groups or one or more conjugated bonds. By "heteroalkyl" herein is meant an alkyl group that has at least one heteroatom, i.e. nitrogen, oxygen, sulfur, phosphorus, silicon or boron included in the chain. Alternatively, the insulator may be quite similar to a conductive oligomer with the addition of one or more heteroatoms or bonds that serve to inhibit or slow, preferably substantially, electron transfer.

Suitable insulators are known in the art, and include, but are not limited to, $-(CH_2)_n-$, $-(CRH)_n-$, and $-(CR_2)_n-$, ethylene glycol or derivatives using other heteroatoms in place of oxygen, i.e. nitrogen or sulfur (sulfur derivatives are not preferred when the electrode is gold).

As for the conductive oligomers, the insulators may be substituted with R groups as defined herein to alter the packing of the moieties or conductive oligomers on an electrode, the hydrophilicity or hydrophobicity of the insulator, and the flexibility, i.e. the rotational, torsional or longitudinal flexibility of the insulator. For example, branched alkyl groups may be used. Similarly, the insulators may contain terminal groups, as outlined above, particularly to influence the surface of the monolayer.

The length of the species making up the monolayer will vary as needed. As outlined above, it appears that binding of target analytes (for example, hybridization of nucleic acids) is more efficient at a distance from the surface. The species to which capture binding ligands are attached (as outlined below, these can be either insulators or conductive oligomers) may be basically the same length as the monolayer forming species or longer than them, resulting in the capture binding ligands being more accessible to the solvent for hybridization. In some embodiments, the conductive oligomers to which the capture binding ligands are attached may be shorter than the monolayer.

As will be appreciated by those in the art, the actual combinations and ratios of the different species making up the monolayer can vary widely, and will depend on whether mechanism-1 or -2 is used. Generally, three component systems are preferred for mechanism-2 systems, with the first species comprising a capture probe containing species, attached to the electrode via either an insulator or a conductive oligomer. The second species are EFS, preferably conductive oligomers, and the third species are insulators. In this embodiment, the first species can comprise from about 90% to about 1%, with from about 20% to about 40% being preferred. For nucleic acids, from about 30% to about 40% is especially preferred for short oligonucleotide targets and from about 10% to about 20% is preferred for longer targets. The second species can comprise from about 1% to about 90%, with from about 20% to about 90% being preferred, and from about 40% to about 60% being especially preferred. The third species can comprise from about 1% to about 90%, with from about 20% to about 40% being preferred, and from about 15% to about 30% being especially preferred. To achieve these approximate proportions, preferred ratios of first:second:third species in SAM formation solvents are 2:2:1 for short targets, 1:3:1 for longer targets, with total thiol concentration (when used to attach these species, as is more fully outlined below) in the 500 μ M to 1 mM range, and 833 μ M being preferred.

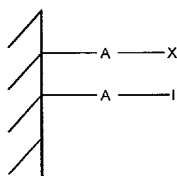
Alternatively, two component systems can be used. In one embodiment, for use in either mechanism-1 or mechanism-2 systems, the two components are the first and second species. In this embodiment, the first species can comprise from about 1% to about 90%, with from about 1% to about 40% being

preferred, and from about 10% to about 40% being especially preferred. The second species can comprise from about 1% to about 90%, with from about 10% to about 60% being preferred, and from about 20% to about 40% being especially preferred. Alternatively, for mechanism-1 systems, the two components are the first and the third species. In this embodiment, the first species can comprise from about 1% to about 90%, with from about 1% to about 40% being preferred, and from about 10% to about 40% being especially preferred. The second species can comprise from about 1% to about 90%, with from about 10% to about 60% being preferred, and from about 20% to about 40% being especially preferred.

In a preferred embodiment, the deposition of the SAM is done using aqueous solvents. As is generally described in Steel et al., *Anal. Chem.* 70:4670 (1998), Herne et al., *J. Am. Chem. Soc.* 119:8916 (1997), and Finklea, *Electrochemistry of Organized Monolayers of Thiols and Related Molecules on Electrodes*, from A.J. Bard, Electroanalytical Chemistry: A Series of Advances, Vol. 20, Dekker N.Y. 1966-, all of which are expressly incorporated by reference, the deposition of the SAM-forming species can be done out of aqueous solutions, frequently comprising salt.

The covalent attachment of the conductive oligomers and insulators to the electrode may be accomplished in a variety of ways, depending on the electrode and the composition of the insulators and conductive oligomers used. In a preferred embodiment, the attachment linkers with covalently attached nucleosides or nucleic acids as depicted herein are covalently attached to an electrode. Thus, one end or terminus of the attachment linker is attached to the nucleoside or nucleic acid, and the other is attached to an electrode. In some embodiments it may be desirable to have the attachment linker attached at a position other than a terminus, or even to have a branched attachment linker that is attached to an electrode at one terminus and to two or more nucleosides at other termini, although this is not preferred. Similarly, the attachment linker may be attached at two sites to the electrode, as is generally depicted in Structures 11-13. Generally, some type of linker is used, as depicted below as "A" in Structure 10, where "X" is the conductive oligomer, "I" is an insulator and the hatched surface is the electrode:

Structure 10

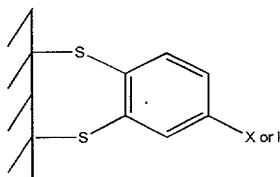


In this embodiment, A is a linker or atom. The choice of "A" will depend in part on the characteristics of the electrode. Thus, for example, A may be a sulfur moiety when a gold electrode is used. Alternatively, when metal oxide electrodes are used, A may be a silicon (silane) moiety attached to the

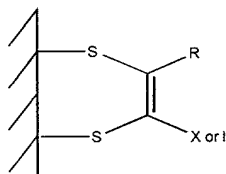
oxygen of the oxide (see for example Chen et al., Langmuir 10:3332-3337 (1994); Lenhard et al., J. Electroanal. Chem. 78:195-201 (1977), both of which are expressly incorporated by reference). When carbon based electrodes are used, A may be an amino moiety (preferably a primary amine; see for example Deinhammer et al., Langmuir 10:1306-1313 (1994)). Thus, preferred A moieties include, but are not limited to, silane moieties, sulfur moieties (including alkyl sulfur moieties), and amino moieties. In a preferred embodiment, epoxide type linkages with redox polymers such as are known in the art are not used.

Although depicted herein as a single moiety, the insulators and conductive oligomers may be attached to the electrode with more than one "A" moiety; the "A" moieties may be the same or different. Thus, for example, when the electrode is a gold electrode, and "A" is a sulfur atom or moiety, multiple sulfur atoms may be used to attach the conductive oligomer to the electrode, such as is generally depicted below in Structures 11, 12 and 13. As will be appreciated by those in the art, other such structures can be made. In Structures 11, 12 and 13, the A moiety is just a sulfur atom, but substituted sulfur moieties may also be used.

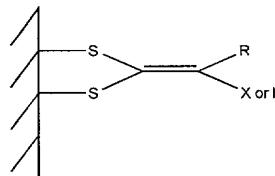
Structure 11



Structure 12



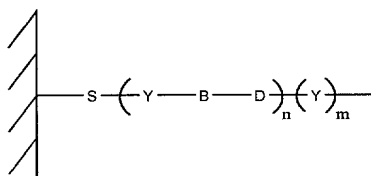
Structure 13



It should also be noted that similar to Structure 13, it may be possible to have a conductive oligomer terminating in a single carbon atom with three sulfur moieties attached to the electrode. Additionally, although not always depicted herein, the conductive oligomers and insulators may also comprise a "Q" terminal group.

In a preferred embodiment, the electrode is a gold electrode, and attachment is via a sulfur linkage as is well known in the art, i.e. the A moiety is a sulfur atom or moiety. Although the exact characteristics of the gold-sulfur attachment are not known, this linkage is considered covalent for the purposes of this invention. A representative structure is depicted in Structure 14, using the Structure 3 conductive oligomer, although as for all the structures depicted herein, any of the conductive oligomers, or combinations of conductive oligomers, may be used. Similarly, any of the conductive oligomers or insulators may also comprise terminal groups as described herein. Structure 14 depicts the "A" linker as comprising just a sulfur atom, although additional atoms may be present (i.e. linkers from the sulfur to the conductive oligomer or substitution groups). In addition, Structure 14 shows the sulfur atom attached to the Y aromatic group, but as will be appreciated by those in the art, it may be attached to the B-D group (i.e. an acetylene) as well.

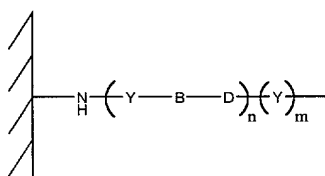
Structure 14



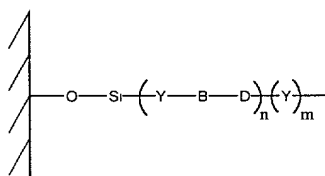
In general, thiol linkages are preferred.

In a preferred embodiment, the electrode is a carbon electrode, i.e. a glassy carbon electrode, and attachment is via a nitrogen of an amine group. A representative structure is depicted in Structure 15. Again, additional atoms may be present, i.e. Z type linkers and/or terminal groups.

Structure 15



Structure 16



In Structure 16, the oxygen atom is from the oxide of the metal oxide electrode. The Si atom may also contain other atoms, i.e. be a silicon moiety containing substitution groups. Other attachments for SAMs to other electrodes are known in the art; see for example Napier et al., Langmuir, 1997, for

attachment to indium tin oxide electrodes, and also the chemisorption of phosphates to an indium tin oxide electrode (talk by H. Holden Thorpe, CHI conference, May 4-5, 1998).

The SAMs of the invention can be made in a variety of ways, including deposition out of organic solutions and deposition out of aqueous solutions. The methods outlined herein use a gold electrode as the example, although as will be appreciated by those in the art, other metals and methods may be used as well. In one preferred embodiment, indium-tin-oxide (ITO) is used as the electrode.

In a preferred embodiment, a gold surface is first cleaned. A variety of cleaning procedures may be employed, including, but not limited to, chemical cleaning or etchants (including Piranha solution (hydrogen peroxide/sulfuric acid) or aqua regia (hydrochloric acid/nitric acid), electrochemical methods, flame treatment, plasma treatment or combinations thereof.

Following cleaning, the gold substrate is exposed to the SAM species. When the electrode is ITO, the SAM species are phosphonate-containing species. This can also be done in a variety of ways, including, but not limited to, solution deposition, gas phase deposition, microcontact printing, spray deposition, deposition using neat components, etc. A preferred embodiment utilizes a deposition solution comprising a mixture of various SAM species in solution, generally thiol-containing species. Mixed monolayers that contain target analytes, particularly DNA, are usually prepared using a two step procedure. The thiolated DNA is deposited during the first deposition step (generally in the presence of at least one other monolayer-forming species) and the mixed monolayer formation is completed during the second step in which a second thiol solution minus DNA is added. The second step frequently involves mild heating to promote monolayer reorganization.

In a preferred embodiment, the deposition solution is an organic deposition solution. In this embodiment, a clean gold surface is placed into a clean vial. A binding ligand deposition solution in organic solvent is prepared in which the total thiol concentration is between micromolar to saturation; preferred ranges include from about 1 μ M to 10 mM, with from about 400 μ M to about 1.0 mM being especially preferred. In a preferred embodiment, the deposition solution contains thiol modified DNA (i.e. nucleic acid attached to an attachment linker) and thiol diluent molecules (either conductive oligomers or insulators, with the latter being preferred). The ratio of DNA to diluent (if present) is usually between 1000:1 to 1:1000, with from about 10:1 to about 1:10 being preferred and 1:1 being especially preferred. The preferred solvents are tetrahydrofuran (THF), acetonitrile, dimethylformamide (DMF), ethanol, or mixtures thereof; generally any solvent of sufficient polarity to dissolve the capture ligand can be used, as long as the solvent is devoid of functional groups that will react with the surface. Sufficient DNA deposition solution is added to the vial so as to completely cover the electrode surface. The gold substrate is allowed to incubate at ambient temperature or slightly above

ambient temperature for a period of time ranging from seconds to hours, with 5-30 minutes being preferred. After the initial incubation, the deposition solution is removed and a solution of diluent molecule only (from about 1 μM to 10 mM, with from about 100 μM to about 1.0 mM being preferred) in organic solvent is added. The gold substrate is allowed to incubate at room temperature or above room temperature for a period of time (seconds to days, with from about 10 minutes to about 24 hours being preferred). The gold sample is removed from the solution, rinsed in clean solvent and used.

In a preferred embodiment, an aqueous deposition solution is used. As above, a clean gold surface is placed into a clean vial. A DNA deposition solution in water is prepared in which the total thiol concentration is between about 1 μM and 10 mM, with from about 1 μM to about 200 μM being preferred. The aqueous solution frequently has salt present (up to saturation, with approximately 1M being preferred), however pure water can be used. The deposition solution contains thiol modified DNA and often a thiol diluent molecule. The ratio of DNA to diluent is usually between between 1000:1 to 1:1000, with from about 10:1 to about 1:10 being preferred and 1:1 being especially preferred. The DNA deposition solution is added to the vial in such a volume so as to completely cover the electrode surface. The gold substrate is allowed to incubate at ambient temperature or slightly above ambient temperature for 1-30 minutes with 5 minutes usually being sufficient. After the initial incubation, the deposition solution is removed and a solution of diluent molecule only (10 μM –1.0 mM) in either water or organic solvent is added. The gold substrate is allowed to incubate at room temperature or above room temperature until a complete monolayer is formed (10 minutes-24 hours). The gold sample is removed from the solution, rinsed in clean solvent and used.

In a preferred embodiment, as outlined herein, a circuit board is used as the substrate for the gold electrodes. Formation of the SAMs on the gold surface is generally done by first cleaning the boards, for example in a 10% sulfuric acid solution for 30 seconds, detergent solutions, aqua regia, plasma, etc., as outlined herein. Following the sulfuric acid treatment, the boards are washed, for example via immersion in two Milli-Q water baths for 1 minute each. The boards are then dried, for example under a stream of nitrogen. Spotting of the deposition solution onto the boards is done using any number of known spotting systems, generally by placing the boards on an X-Y table, preferably in a humidity chamber. The size of the spotting drop will vary with the size of the electrodes on the boards and the equipment used for delivery of the solution; for example, for 250 μM size electrodes, a 30 nanoliter drop is used. The volume should be sufficient to cover the electrode surface completely. The drop is incubated at room temperature for a period of time (sec to overnight, with 5 minutes preferred) and then the drop is removed by rinsing in a Milli-Q water bath. The boards are then preferably treated with a second deposition solution, generally comprising insulator in organic solvent, preferably acetonitrile, by immersion in a 45°C bath. After 30 minutes, the boards are removed and immersed in

an acetonitrile bath for 30 seconds followed by a milli-Q water bath for 30 seconds. The boards are dried under a stream of nitrogen.

In a preferred embodiment, the detection electrode further comprises a capture binding ligand, preferably covalently attached. By "binding ligand" or "binding species" herein is meant a compound that is used to probe for the presence of the target analyte, that will bind to the target analyte. In general, for most of the embodiments described herein, there are at least two binding ligands used per target analyte molecule; a "capture" or "anchor" binding ligand (also referred to herein as a "capture probe", particularly in reference to a nucleic acid binding ligand) that is attached to the detection electrode as described herein, and a soluble binding ligand, that binds independently to the target analyte, and either directly or indirectly comprises at least one ETM.

Generally, the capture binding ligand allows the attachment of a target analyte to the detection electrode, for the purposes of detection. As is more fully outlined below, attachment of the target analyte to the capture binding ligand may be direct (i.e. the target analyte binds to the capture binding ligand) or indirect (one or more capture extender ligands may be used).

In a preferred embodiment, the binding is specific, and the binding ligand is part of a binding pair. By "specifically bind" herein is meant that the ligand binds the analyte, with specificity sufficient to differentiate between the analyte and other components or contaminants of the test sample. However, as will be appreciated by those in the art, it will be possible to detect analytes using binding that is not highly specific; for example, the systems may use different binding ligands, for example an array of different ligands, and detection of any particular analyte is via its "signature" of binding to a panel of binding ligands, similar to the manner in which "electronic noses" work. The binding should be sufficient to allow the analyte to remain bound under the conditions of the assay, including wash steps to remove non-specific binding. In some embodiments, for example in the detection of certain biomolecules, the binding constants of the analyte to the binding ligand will be at least about 10^{-4} to 10^{-6} M⁻¹, with at least about 10^{-5} to 10^{-9} being preferred and at least about 10^{-7} to 10^{-9} M⁻¹ being particularly preferred.

As will be appreciated by those in the art, the composition of the binding ligand will depend on the composition of the target analyte. Binding ligands to a wide variety of analytes are known or can be readily found using known techniques. For example, when the analyte is a single-stranded nucleic acid, the binding ligand is generally a substantially complementary nucleic acid. Alternatively, as is generally described in U.S. Patents 5,270,163, 5,475,096, 5,567,588, 5,595,877, 5,637,459, 5,683,867, 5,705,337, and related patents, hereby incorporated by reference, nucleic acid "aptomers" can be developed for binding to virtually any target analyte. Similarly the analyte may be a nucleic

acid binding protein and the capture binding ligand is either a single-stranded or double-stranded nucleic acid; alternatively, the binding ligand may be a nucleic acid binding protein when the analyte is a single or double-stranded nucleic acid. When the analyte is a protein, the binding ligands include proteins (particularly including antibodies or fragments thereof (FABs, etc.)), small molecules, or aptamers, described above. Preferred binding ligand proteins include peptides. For example, when the analyte is an enzyme, suitable binding ligands include substrates, inhibitors, and other proteins that bind the enzyme, i.e. components of a multi-enzyme (or protein) complex. As will be appreciated by those in the art, any two molecules that will associate, preferably specifically, may be used, either as the analyte or the binding ligand. Suitable analyte/binding ligand pairs include, but are not limited to, antibodies/antigens, receptors/ligand, proteins/nucleic acids; nucleic acids/nucleic acids, enzymes/substrates and/or inhibitors, carbohydrates (including glycoproteins and glycolipids)/lectins, carbohydrates and other binding partners, proteins/proteins; and protein/small molecules. These may be wild-type or derivative sequences. In a preferred embodiment, the binding ligands are portions (particularly the extracellular portions) of cell surface receptors that are known to multimerize, such as the growth hormone receptor, glucose transporters (particularly GLUT4 receptor), transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, high density lipoprotein receptor, leptin receptor, interleukin receptors including IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-11, IL-12, IL-13, IL-15 and IL-17 receptors, VEGF receptor, PDGF receptor, EPO receptor, TPO receptor, ciliary neurotrophic factor receptor, prolactin receptor, and T-cell receptors. Similarly, there is a wide body of literature relating to the development of binding partners based on combinatorial chemistry methods.

In this embodiment, when the binding ligand is a nucleic acid, preferred compositions and techniques are outlined in WO 98/20162; PCT/US98/12430; PCT/US98/12082; PCT/US99/01705; PCT/US99/01703; and U.S.S.N.s 09/135,183; 60/105,875; and 09/295,691, all of which are hereby expressly incorporated by reference.

The method of attachment of the capture binding ligands to the attachment linker (either an insulator or conductive oligomer) will generally be done as is known in the art, and will depend on both the composition of the attachment linker and the capture binding ligand. In general, the capture binding ligands are attached to the attachment linker through the use of functional groups on each that can then be used for attachment. Preferred functional groups for attachment are amino groups, carboxy groups, oxo groups and thiol groups. These functional groups can then be attached, either directly or indirectly through the use of a linker, sometimes depicted herein as "Z". Linkers are well known in the art; for example, homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference). Preferred Z linkers include, but are not limited to, alkyl groups (including substituted alkyl

groups and alkyl groups containing heteroatom moieties), with short alkyl groups, esters, amide, amine, epoxy groups and ethylene glycol and derivatives being preferred, with propyl, acetylene, and C₂ alkene being especially preferred. Z may also be a sulfone group, forming sulfonamide linkages.

In this way, capture binding ligands comprising proteins, lectins, nucleic acids, small organic molecules, carbohydrates, etc. can be added.

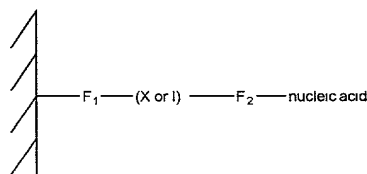
A preferred embodiment utilizes proteinaceous capture binding ligands. As is known in the art, any number of techniques may be used to attach a proteinaceous capture binding ligand to an attachment linker. A wide variety of techniques are known to add moieties to proteins.

A preferred embodiment utilizes nucleic acids as the capture binding ligand. While most of the following discussion focuses on nucleic acids, as will be appreciated by those in the art, many of the techniques outlined below apply in a similar manner to non-nucleic acid systems as well.

The capture probe nucleic acid is covalently attached to the electrode, via an "attachment linker", that can be either a conductive oligomer (required for mechanism-1 systems) or an insulator. By "covalently attached" herein is meant that two moieties are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds.

Thus, one end of the attachment linker is attached to a nucleic acid (or other binding ligand), and the other end (although as will be appreciated by those in the art, it need not be the exact terminus for either) is attached to the electrode. Thus, any of structures depicted herein may further comprise a nucleic acid effectively as a terminal group. Thus, the present invention provides compositions comprising nucleic acids covalently attached to electrodes as is generally depicted below in Structure 17:

Structure 17



In Structure 17, the hatched marks on the left represent an electrode. X is a conductive oligomer and I is an insulator as defined herein. F₁ is a linkage that allows the covalent attachment of the electrode and the conductive oligomer or insulator, including bonds, atoms or linkers such as is described herein, for example as "A", defined below. F₂ is a linkage that allows the covalent attachment of the conductive oligomer or insulator to the nucleic acid, and may be a bond, an atom or a linkage as is

herein described. F_2 may be part of the conductive oligomer, part of the insulator, part of the nucleic acid, or exogeneous to both, for example, as defined herein for "Z".

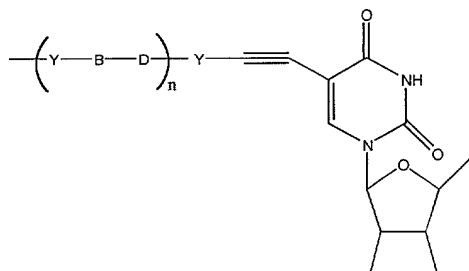
In a preferred embodiment, the capture probe nucleic acid is covalently attached to the electrode via a conductive oligomer. The covalent attachment of the nucleic acid and the conductive oligomer may be accomplished in several ways. In a preferred embodiment, the attachment is via attachment to the base of the nucleoside, via attachment to the backbone of the nucleic acid (either the ribose, the phosphate, or to an analogous group of a nucleic acid analog backbone), or via a transition metal ligand, as described below. The techniques outlined below are generally described for naturally occurring nucleic acids, although as will be appreciated by those in the art, similar techniques may be used with nucleic acid analogs, and in some cases with other binding ligands.

In a preferred embodiment, the conductive oligomer is attached to the base of a nucleoside of the nucleic acid. This may be done in several ways, depending on the oligomer, as is described below. In one embodiment, the oligomer is attached to a terminal nucleoside, i.e. either the 3' or 5' nucleoside of the nucleic acid. Alternatively, the conductive oligomer is attached to an internal nucleoside.

The point of attachment to the base will vary with the base. Generally, attachment at any position is possible. In some embodiments, for example when the probe containing the ETMs may be used for hybridization (i.e. mechanism-1 systems), it is preferred to attach at positions not involved in hydrogen bonding to the complementary base. Thus, for example, generally attachment is to the 5 or 6 position of pyrimidines such as uridine, cytosine and thymine. For purines such as adenine and guanine, the linkage is preferably via the 8 position. Attachment to non-standard bases is preferably done at the comparable positions.

In one embodiment, the attachment is direct; that is, there are no intervening atoms between the conductive oligomer and the base. In this embodiment, for example, conductive oligomers with terminal acetylene bonds are attached directly to the base. Structure 18 is an example of this linkage, using a Structure 3 conductive oligomer and uridine as the base, although other bases and conductive oligomers can be used as will be appreciated by those in the art:

Structure 18

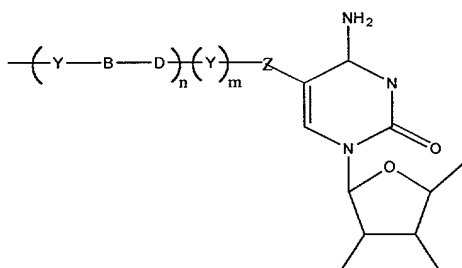


It should be noted that the pentose structures depicted herein may have hydrogen, hydroxy, phosphates or other groups such as amino groups attached. In addition, the pentose and nucleoside structures depicted herein are depicted non-conventionally, as mirror images of the normal rendering. In addition, the pentose and nucleoside structures may also contain additional groups, such as protecting groups, at any position, for example as needed during synthesis.

In addition, the base may contain additional modifications as needed, i.e. the carbonyl or amine groups may be altered or protected.

In an alternative embodiment, the attachment is any number of different Z linkers, including amide and amine linkages, as is generally depicted in Structure 19 using uridine as the base and a Structure 3 oligomer:

Structure 19:



In this embodiment, Z is a linker. Preferably, Z is a short linker of about 1 to about 10 atoms, with from 1 to 5 atoms being preferred, that may or may not contain alkene, alkynyl, amine, amide, azo, imine, etc., bonds. Linkers are known in the art; for example, homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference). Preferred Z linkers include, but are not limited to, alkyl groups (including substituted alkyl groups and alkyl groups containing heteroatom moieties), with short alkyl groups, esters, amide, amine, epoxy groups and ethylene glycol and derivatives being preferred, with propyl, acetylene, and C₂ alkene being especially preferred. Z may also be a sulfone group, forming sulfonamide linkages as discussed below.

In a preferred embodiment, the attachment of the nucleic acid and the conductive oligomer is done via attachment to the backbone of the nucleic acid. This may be done in a number of ways, including attachment to a ribose of the ribose-phosphate backbone, or to the phosphate of the backbone, or other groups of analogous backbones.

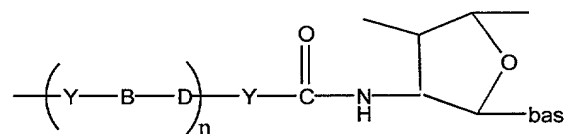
As a preliminary matter, it should be understood that the site of attachment in this embodiment may be to a 3' or 5' terminal nucleotide, or to an internal nucleotide, as is more fully described below.

In a preferred embodiment, the conductive oligomer is attached to the ribose of the ribose-phosphate backbone. This may be done in several ways. As is known in the art, nucleosides that are modified at either the 2' or 3' position of the ribose with amino groups, sulfur groups, silicone groups, phosphorus groups, or oxo groups can be made (Imazawa et al., J. Org. Chem., 44:2039 (1979); Hobbs et al., J. Org. Chem. 42(4):714 (1977); Verheyden et al., J. Org. Chem. 36(2):250 (1971); McGee et al., J. Org. Chem. 61:781-785 (1996); Mikhailopulo et al., Liebigs. Ann. Chem. 513-519 (1993); McGee et al., Nucleosides & Nucleotides 14(6):1329 (1995), all of which are incorporated by reference). These modified nucleosides are then used to add the conductive oligomers.

A preferred embodiment utilizes amino-modified nucleosides. These amino-modified riboses can then be used to form either amide or amine linkages to the conductive oligomers. In a preferred embodiment, the amino group is attached directly to the ribose, although as will be appreciated by those in the art, short linkers such as those described herein for "Z" may be present between the amino group and the ribose.

In a preferred embodiment, an amide linkage is used for attachment to the ribose. Preferably, if the conductive oligomer of Structures 1-3 is used, m is zero and thus the conductive oligomer terminates in the amide bond. In this embodiment, the nitrogen of the amino group of the amino-modified ribose is the "D" atom of the conductive oligomer. Thus, a preferred attachment of this embodiment is depicted in Structure 20 (using the Structure 3 conductive oligomer):

Structure 20

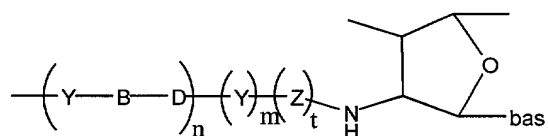


As will be appreciated by those in the art, Structure 20 has the terminal bond fixed as an amide bond.

In a preferred embodiment, a heteroatom linkage is used, i.e. oxo, amine, sulfur, etc. A preferred embodiment utilizes an amine linkage. Again, as outlined above for the amide linkages, for amine

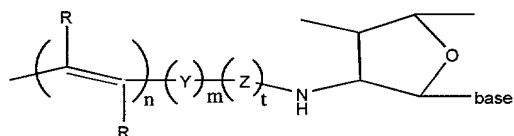
linkages, the nitrogen of the amino-modified ribose may be the "D" atom of the conductive oligomer when the Structure 3 conductive oligomer is used. Thus, for example, Structures 21 and 22 depict nucleosides with the Structures 3 and 9 conductive oligomers, respectively, using the nitrogen as the heteroatom, although other heteroatoms can be used:

Structure 21



In Structure 21, preferably both m and t are not zero. A preferred Z here is a methylene group, or other aliphatic alkyl linkers. One, two or three carbons in this position are particularly useful for synthetic reasons.

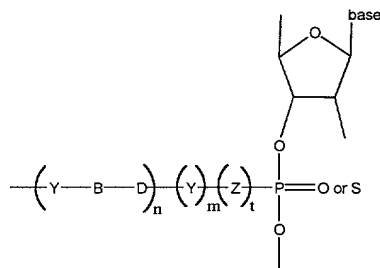
Structure 22



In Structure 22, Z is as defined above. Suitable linkers include methylene and ethylene.

In an alternative embodiment, the conductive oligomer is covalently attached to the nucleic acid via the phosphate of the ribose-phosphate backbone (or analog) of a nucleic acid. In this embodiment, the attachment is direct, utilizes a linker or via an amide bond. Structure 23 depicts a direct linkage, and Structure 24 depicts linkage via an amide bond (both utilize the Structure 3 conductive oligomer, although Structure 8 conductive oligomers are also possible). Structures 23 and 24 depict the conductive oligomer in the 3' position, although the 5' position is also possible. Furthermore, both Structures 23 and 24 depict naturally occurring phosphodiester bonds, although as those in the art will appreciate, non-standard analogs of phosphodiester bonds may also be used.

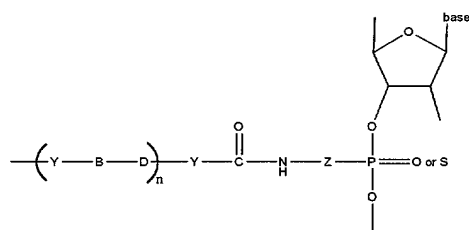
Structure 23



In Structure 23, if the terminal Y is present (i.e. m=1), then preferably Z is not present (i.e. t=0). If the terminal Y is not present, then Z is preferably present.

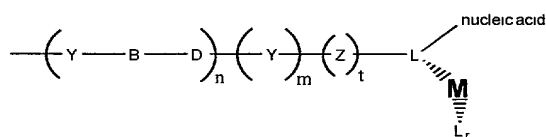
Structure 24 depicts a preferred embodiment, wherein the terminal B-D bond is an amide bond, the terminal Y is not present, and Z is a linker, as defined herein.

Structure 24

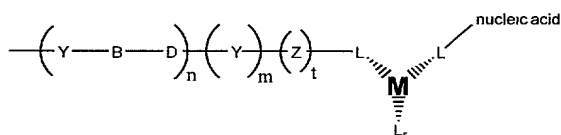


In a preferred embodiment, the conductive oligomer is covalently attached to the nucleic acid via a transition metal ligand. In this embodiment, the conductive oligomer is covalently attached to a ligand which provides one or more of the coordination atoms for a transition metal. In one embodiment, the ligand to which the conductive oligomer is attached also has the nucleic acid attached, as is generally depicted below in Structure 25. Alternatively, the conductive oligomer is attached to one ligand, and the nucleic acid is attached to another ligand, as is generally depicted below in Structure 26. Thus, in the presence of the transition metal, the conductive oligomer is covalently attached to the nucleic acid. Both of these structures depict Structure 3 conductive oligomers, although other oligomers may be utilized. Structures 25 and 26 depict two representative structures:

Structure 25



Structure 26



In the structures depicted herein, M is a metal atom, with transition metals being preferred. Suitable transition metals for use in the invention include, but are not limited to, cadmium (Cd), copper (Cu), cobalt (Co), palladium (Pd), zinc (Zn), iron (Fe), ruthenium (Ru), rhodium (Rh), osmium (Os), rhenium (Re), platinum (Pt), scandium (Sc), titanium (Ti), Vanadium (V), chromium (Cr), manganese (Mn), nickel (Ni), Molybdenum (Mo), technetium (Tc), tungsten (W), and iridium (Ir). That is, the first series of transition metals, the platinum metals (Ru, Rh, Pd, Os, Ir and Pt), along with Fe, Re, W, Mo and Tc, are preferred. Particularly preferred are ruthenium, rhenium, osmium, platinum, cobalt and iron.

L are the co-ligands, that provide the coordination atoms for the binding of the metal ion. As will be appreciated by those in the art, the number and nature of the co-ligands will depend on the coordination number of the metal ion. Mono-, di- or polydentate co-ligands may be used at any position. Thus, for example, when the metal has a coordination number of six, the L from the terminus of the conductive oligomer, the L contributed from the nucleic acid, and r, add up to six. Thus, when the metal has a coordination number of six, r may range from zero (when all coordination atoms are provided by the other two ligands) to four, when all the co-ligands are monodentate. Thus generally, r will be from 0 to 8, depending on the coordination number of the metal ion and the choice of the other ligands.

In one embodiment, the metal ion has a coordination number of six and both the ligand attached to the conductive oligomer and the ligand attached to the nucleic acid are at least bidentate; that is, r is preferably zero, one (i.e. the remaining co-ligand is bidentate) or two (two monodentate co-ligands are used).

As will be appreciated in the art, the co-ligands can be the same or different. Suitable ligands fall into two categories: ligands which use nitrogen, oxygen, sulfur, carbon or phosphorus atoms (depending on the metal ion) as the coordination atoms (generally referred to in the literature as sigma (σ) donors) and organometallic ligands such as metallocene ligands (generally referred to in the literature as pi (π) donors, and depicted herein as L_m). Suitable nitrogen donating ligands are well known in the art and include, but are not limited to, NH_2 ; NHR; NRR' ; pyridine; pyrazine; isonicotinamide; imidazole; bipyridine and substituted derivatives of bipyridine; terpyridine and substituted derivatives; phenanthrolines, particularly 1,10-phenanthroline (abbreviated phen) and substituted derivatives of phenanthrolines such as 4,7-dimethylphenanthroline and dipyrldol[3,2-a:2',3'-c]phenazine (abbreviated dppz); dipyrldophenazine; 1,4,5,8,9,12-hexaazatriphenylene (abbreviated hat); 9,10-phenanthrenequinone diimine (abbreviated phi); 1,4,5,8-tetraazaphenanthrene (abbreviated tap); 1,4,8,11-tetra-azacyclotetradecane (abbreviated cyclam), EDTA, EGTA and isocyanide. Substituted derivatives, including fused derivatives, may also be used. In some embodiments, porphyrins and substituted derivatives of the porphyrin family may be used. See for example, Comprehensive Coordination Chemistry, Ed. Wilkinson et al., Pergamon Press, 1987, Chapters 13.2 (pp73-98), 21.1 (pp. 813-898) and 21.3 (pp 915-957), all of which are hereby expressly incorporated by reference.

Suitable sigma donating ligands using carbon, oxygen, sulfur and phosphorus are known in the art. For example, suitable sigma carbon donors are found in Cotton and Wilkenson, Advanced Organic Chemistry, 5th Edition, John Wiley & Sons, 1988, hereby incorporated by reference; see page 38, for example. Similarly, suitable oxygen ligands include crown ethers, water and others known in the art. Phosphines and substituted phosphines are also suitable; see page 38 of Cotton and Wilkenson.

The oxygen, sulfur, phosphorus and nitrogen-donating ligands are attached in such a manner as to allow the heteroatoms to serve as coordination atoms.

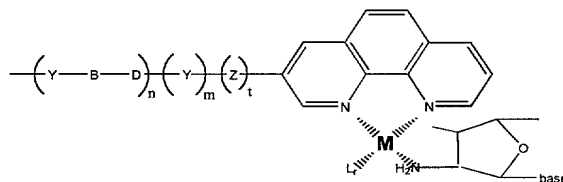
In a preferred embodiment, organometallic ligands are used. In addition to purely organic compounds for use as redox moieties, and various transition metal coordination complexes with δ -bonded organic ligand with donor atoms as heterocyclic or exocyclic substituents, there is available a wide variety of transition metal organometallic compounds with π -bonded organic ligands (see Advanced Inorganic Chemistry, 5th Ed., Cotton & Wilkinson, John Wiley & Sons, 1988, chapter 26; Organometallics, A Concise Introduction, Elschenbroich et al., 2nd Ed., 1992, VCH; and Comprehensive Organometallic Chemistry II, A Review of the Literature 1982-1994, Abel et al. Ed., Vol. 7, chapters 7, 8, 10 & 11, Pergamon Press, hereby expressly incorporated by reference). Such organometallic ligands include cyclic aromatic compounds such as the cyclopentadienide ion $[C_5H_5(-1)]$ and various ring substituted and ring fused derivatives, such as the indenylide (-1) ion, that yield a class of bis(cyclopentadienyl) metal compounds, (i.e. the metallocenes); see for example Robins et al., J. Am. Chem. Soc. 104:1882-1893 (1982); and Gassman et al., J. Am. Chem. Soc. 108:4228-4229 (1986), incorporated by reference. Of these, ferrocene $[(C_5H_5)_2Fe]$ and its derivatives are prototypical examples which have been used in a wide variety of chemical (Connelly et al., Chem. Rev. 96:877-910 (1996), incorporated by reference) and electrochemical (Geiger et al., Advances in Organometallic Chemistry 23:1-93; and Geiger et al., Advances in Organometallic Chemistry 24:87, incorporated by reference) electron transfer or "redox" reactions. Metallocene derivatives of a variety of the first, second and third row transition metals are potential candidates as redox moieties that are covalently attached to either the ribose ring or the nucleoside base of nucleic acid. Other potentially suitable organometallic ligands include cyclic arenes such as benzene, to yield bis(arene)metal compounds and their ring substituted and ring fused derivatives, of which bis(benzene)chromium is a prototypical example. Other acyclic π -bonded ligands such as the allyl (-1) ion, or butadiene yield potentially suitable organometallic compounds, and all such ligands, in conjunction with other π -bonded and δ -bonded ligands constitute the general class of organometallic compounds in which there is a metal to carbon bond. Electrochemical studies of various dimers and oligomers of such compounds with bridging organic ligands, and additional non-bridging ligands, as well as with and without metal-metal bonds are potential candidate redox moieties in nucleic acid analysis.

When one or more of the co-ligands is an organometallic ligand, the ligand is generally attached via one of the carbon atoms of the organometallic ligand, although attachment may be via other atoms for heterocyclic ligands. Preferred organometallic ligands include metallocene ligands, including substituted derivatives and the metalloceneophanes (see page 1174 of Cotton and Wilkenson, supra). For example, derivatives of metallocene ligands such as methylcyclopentadienyl, with multiple methyl groups being preferred, such as pentamethylcyclopentadienyl, can be used to increase the stability of

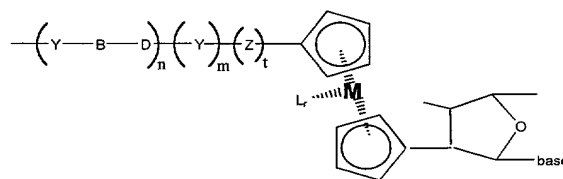
the metallocene. In a preferred embodiment, only one of the two metallocene ligands of a metallocene are derivatized.

As described herein, any combination of ligands may be used. Preferred combinations include: a) all ligands are nitrogen donating ligands; b) all ligands are organometallic ligands; and c) the ligand at the terminus of the conductive oligomer is a metallocene ligand and the ligand provided by the nucleic acid is a nitrogen donating ligand, with the other ligands, if needed, are either nitrogen donating ligands or metallocene ligands, or a mixture. These combinations are depicted in representative structures using the conductive oligomer of Structure 3 are depicted in Structures 27 (using phenanthroline and amino as representative ligands), 28 (using ferrocene as the metal-ligand combination) and 29 (using cyclopentadienyl and amino as representative ligands).

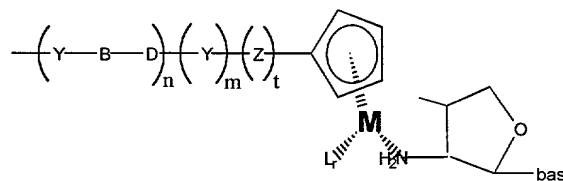
Structure 27



Structure 28



Structure 29



In addition to serving as attachments for conductive oligomers and electrodes, the above compositions can also be used as ETM labels. That is, as is outlined in Figures 19 and 20, transition metals (or other ETMs) attached to conductive oligomers can be added to the nucleic acids for detection. In this embodiment, without being bound by theory, the conductive oligomer, terminating preferably in an F1 linkage (a linkage that allows the attachment of the conductive oligomer to the surface), will penetrate the SAM and facilitate electron transfer between the ETM and the electrode. Without being bound by theory, this appears to allow rapid electron transfer, similar to a "mechanism-1" system, by providing a direct pathway for electrons; this is sometimes referred to herein as "hardwiring".

Surprisingly, as outlined in Example 3, the system appears to work whether or not the F1 moiety is protected; that is, a direct attachment may not be required to increase the frequency response of the ETM. Thus, the conductive oligomer can terminate either in an F1 moiety, an F1 moiety protected with a protecting group (see Greene, *supra*), or need not terminate in an F1 moiety at all; terminal groups such as are used on the surfaces of the SAMs may also be used. Alternatively, the bare terminus of the conductive oligomer may be sufficient.

In this embodiment, a plurality of ETMs per "branch" may be used. They may be attached as a group, e.g. as a metallocene polymer, terminating in the conductive oligomer, or may be substitution groups off of the conductive oligomer. In general, preferred embodiments utilize electronic conjugation between the ETMs and the conductive oligomer, to facilitate electron transfer, or at least minimize the number of non-conjugated bonds.

In general, the length of the conductive oligomer in this embodiment will vary with the length of the SAM on the electrode, and preferred embodiments utilize two unit and three unit oligomers. Preferred conductive oligomers in this embodiment are the same as those outlined above for attachment of nucleic acids to electrodes, with phenyl-acetylene oligomers being the most preferred.

In this embodiment, the ETM with the attached conductive oligomer is generally synthesized, and then a phosphoramidite moiety is made, as is generally depicted in Figure 20.

In a preferred embodiment, the ligands used in the invention show altered fluorescent properties depending on the redox state of the chelated metal ion. As described below, this thus serves as an additional mode of detection of electron transfer between the ETM and the electrode.

In a preferred embodiment, as is described more fully below, the ligand attached to the nucleic acid is an amino group attached to the 2' or 3' position of a ribose of the ribose-phosphate backbone. This ligand may contain a multiplicity of amino groups so as to form a polydentate ligand which binds the metal ion. Other preferred ligands include cyclopentadiene and phenanthroline.

The use of metal ions to connect the nucleic acids can serve as an internal control or calibration of the system, to evaluate the number of available nucleic acids on the surface. However, as will be appreciated by those in the art, if metal ions are used to connect the nucleic acids to the conductive oligomers, it is generally desirable to have this metal ion complex have a different redox potential than that of the ETMs used in the rest of the system, as described below. This is generally true so as to be able to distinguish the presence of the capture probe from the presence of the target sequence. This may be useful for identification, calibration and/or quantification. Thus, the amount of capture probe

on an electrode may be compared to the amount of hybridized double stranded nucleic acid to quantify the amount of target sequence in a sample. This is quite significant to serve as an internal control of the sensor or system. This allows a measurement either prior to the addition of target or after, on the same molecules that will be used for detection, rather than rely on a similar but different control system. Thus, the actual molecules that will be used for the detection can be quantified prior to any experiment. This is a significant advantage over prior methods.

In a preferred embodiment, the capture probe nucleic acids are covalently attached to the electrode via an insulator. The attachment of nucleic acids to insulators such as alkyl groups is well known, and can be done to the base or the backbone, including the ribose or phosphate for backbones containing these moieties, or to alternate backbones for nucleic acid analogs.

In a preferred embodiment, there may be one or more different capture probe species on the surface, as is generally depicted in the Figures. In some embodiments, there may be one type of capture probe, or one type of capture probe extender, as is more fully described below. Alternatively, different capture probes, or one capture probes with a multiplicity of different capture extender probes can be used. Similarly, it may be desirable to use auxillary capture probes that comprise relatively short probe sequences, that can be used to "tack down" components of the system, for example the recruitment linkers, to increase the concentration of ETMs at the surface.

Thus the present invention provides electrodes comprising monolayers comprising conductive oligomers and capture probes, useful in nucleic acid detection systems. In a preferred embodiment, the compositions further comprise a label probe. The label probe is nucleic acid, generally single stranded, although as more fully outlined below, it may contain double-stranded portions. The label probe comprises a first portion that is capable of hybridizing to a component of the assay complex, defined below, and a second portion that does not hybridize to a component of an assay complex and comprises at least one covalently attached ETM.

Thus, label probes with covalently attached ETMs are provided. The terms "electron donor moiety", "electron acceptor moiety", and "ETMs" (ETMs) or grammatical equivalents herein refers to molecules capable of electron transfer under certain conditions. It is to be understood that electron donor and acceptor capabilities are relative; that is, a molecule which can lose an electron under certain experimental conditions will be able to accept an electron under different experimental conditions. It is to be understood that the number of possible electron donor moieties and electron acceptor moieties is very large, and that one skilled in the art of electron transfer compounds will be able to utilize a number of compounds in the present invention. Preferred ETMs include, but are not limited to, transition metal complexes, organic ETMs, and electrodes.

In a preferred embodiment, the ETMs are transition metal complexes. Transition metals are those whose atoms have a partial or complete d shell of electrons. Suitable transition metals for use in the invention are listed above.

The transition metals are complexed with a variety of ligands, L, defined above, to form suitable transition metal complexes, as is well known in the art.

In addition to transition metal complexes, other organic electron donors and acceptors may be covalently attached to the nucleic acid for use in the invention. These organic molecules include, but are not limited to, riboflavin, xanthene dyes, azine dyes, acridine orange, *N,N'*-dimethyl-2,7-diazapyrenium dichloride (DAP²⁺), methylviologen, ethidium bromide, quinones such as *N,N'*-dimethylantra(2,1,9-*def*:6,5,10-*d'e'f'*)diisoquinoline dichloride (ADIQ²⁺); porphyrins ([meso-tetrakis(*N*-methyl-*x*-pyridinium)porphyrin tetrachloride], varlamine blue B hydrochloride, Bindschedler's green; 2,6-dichloroindophenol, 2,6-dibromophenolindophenol; Brilliant crest blue (3-amino-9-dimethyl-amino-10-methylphenoxyazine chloride), methylene blue; Nile blue A (aminoaphthodiethylaminophenoxazine sulfate), indigo-5,5',7,7'-tetrasulfonic acid, indigo-5,5',7-trisulfonic acid; phenosafranine, indigo-5-monosulfonic acid; safranine T; bis(dimethylglyoximate)-iron(II) chloride; induline scarlet, neutral red, anthracene, coronene, pyrene, 9-phenylanthracene, rubrene, binaphthyl, DPA, phenothiazene, fluoranthene, phenanthrene, chrysene, 1,8-diphenyl-1,3,5,7-octatetracene, naphthalene, acenaphthalene, perylene, TMPD and analogs and substituted derivatives of these compounds.

In a preferred embodiment, the ETM may be inherent to the target analyte, or other components of the assay complex that bound to the target analyte. For example, the guanine bases of nucleic acids (which would include target sequences and secondary probes) can be oxidized and may serve as ETMs; see PCT WO97/01646 and U.S. Patent No. 5,871,918, all of which are expressly incorporated by reference. Similarly, many of the electrochemical techniques outlined herein are useful in other systems; see U.S. Patent No. 5,650,061; Singhai et al., *Anal. Chem.* 69:1552 (1997); Singhal and Kuhr, *Anal. Chem.* 69:4828 (1997); Singhal et al., *Anal. Chem.* 69:3553 (1997); and Dontha et al., *Anal. Chem.* 69:2619 (1997), all of which are expressly incorporated by reference herein. In this system, the ribose moieties of the nucleic acids are oxidized and serve as the ETM for the assay. The electrochemical techniques outlined herein may be particularly useful in these systems. Similarly, redox active amino acids may serve as the ETMs in the detection of proteins.

In one embodiment, the electron donors and acceptors are redox proteins as are known in the art. However, redox proteins in many embodiments are not preferred.

The choice of the specific ETMs will be influenced by the type of electron transfer detection used, as is generally outlined below. Preferred ETMs are metallocenes, with ferrocene being particularly preferred.

Without being bound by theory, it appears that in "mechanism-2" systems, electron transfer is facilitated when the ETM is able to penetrate ("snuggle") into the monolayer to some degree. That is, in general, it appears that hydrophobic ETMs used with hydrophobic SAMs give rise to better (greater) signals than ETMs that are charged or more hydrophilic. Thus, for example, ferrocene in solution can penetrate the monolayers of the examples and give a signal when electroconduits are present, while ferrocyanide in solution gives little or no signal. Thus, in general, hydrophobic ETMs are preferred in mechanism-2 systems; however, transition metal complexes, although charged, with one or more hydrophobic ligands, such as bipyridine or phenanthroline, such as Ru and Os complexes, also give rise to good signals. Similarly, electron transfer between the ETM and the electrode is facilitated by the use of linkers or spacers that allow the ETM some flexibility to penetrate into the monolayer; thus the N6 compositions of the invention have a four carbon linker attaching the ETM to the nucleic acid.

In a preferred embodiment, a plurality of ETMs are used. As is shown in the examples, the use of multiple ETMs provides signal amplification and thus allows more sensitive detection limits. As discussed below, while the use of multiple ETMs on nucleic acids that hybridize to complementary strands can cause decreases in T_m s of the hybridization complexes depending on the number, site of attachment and spacing between the multiple ETMs, this is not a factor when the ETMs are on the recruitment linker, since this does not hybridize to a complementary sequence. Accordingly, pluralities of ETMs are preferred, with at least about 2 ETMs per recruitment linker being preferred, and at least about 10 being particularly preferred, and at least about 20 to 50 being especially preferred. In some instances, very large numbers of ETMs (100 to 1000) can be used.

As will be appreciated by those in the art, the portion of the label probe (or target, in some embodiments) that comprises the ETMs (termed herein a "recruitment linker" or "signal carrier") can be nucleic acid, or it can be a non-nucleic acid linker that links the first hybridizable portion of the label probe to the ETMs. That is, since this portion of the label probe is not required for hybridization, it need not be nucleic acid, although this may be done for ease of synthesis. In some embodiments, as is more fully outlined below, the recruitment linker may comprise double-stranded portions. Thus, as will be appreciated by those in the art, there are a variety of configurations that can be used. In a preferred embodiment, the recruitment linker is nucleic acid (including analogs), and attachment of the ETMs can be via (1) a base; (2) the backbone, including the ribose, the phosphate, or comparable structures in nucleic acid analogs; (3) nucleoside replacement, described below; or (4) metallocene polymers, as described below. In a preferred embodiment, the recruitment linker is non-nucleic acid,

and can be either a metallocene polymer or an alkyl-type polymer (including heteroalkyl, as is more fully described below) containing ETM substitution groups. These options are generally depicted in the Figures.

In a preferred embodiment, the recruitment linker is a nucleic acid, and comprises covalently attached ETMs. The ETMs may be attached to nucleosides within the nucleic acid in a variety of positions. Preferred embodiments include, but are not limited to, (1) attachment to the base of the nucleoside, (2) attachment of the ETM as a base replacement, (3) attachment to the backbone of the nucleic acid, including either to a ribose of the ribose-phosphate backbone or to a phosphate moiety, or to analogous structures in nucleic acid analogs, and (4) attachment via metallocene polymers, with the latter being preferred.

In addition, as is described below, when the recruitment linker is nucleic acid, it may be desirable to use secondary label probes, that have a first portion that will hybridize to a portion of the primary label probes and a second portion comprising a recruitment linker as is defined herein. This is generally depicted in Figure 16H; this is similar to the use of an amplifier probe, except that both the primary and the secondary label probes comprise ETMs.

In a preferred embodiment, the ETM is attached to the base of a nucleoside as is generally outlined above for attachment of the conductive oligomer. Attachment can be to an internal nucleoside or a terminal nucleoside.

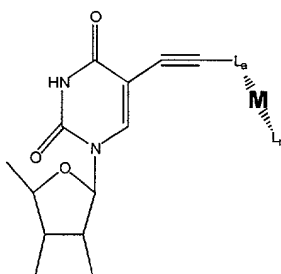
The covalent attachment to the base will depend in part on the ETM chosen, but in general is similar to the attachment of conductive oligomers to bases, as outlined above. Attachment may generally be done to any position of the base. In a preferred embodiment, the ETM is a transition metal complex, and thus attachment of a suitable metal ligand to the base leads to the covalent attachment of the ETM. Alternatively, similar types of linkages may be used for the attachment of organic ETMs, as will be appreciated by those in the art.

In one embodiment, the C4 attached amino group of cytosine, the C6 attached amino group of adenine, or the C2 attached amino group of guanine may be used as a transition metal ligand.

Ligands containing aromatic groups can be attached via acetylene linkages as is known in the art (see Comprehensive Organic Synthesis, Trost et al., Ed., Pergamon Press, Chapter 2.4: Coupling Reactions Between sp^2 and sp Carbon Centers, Sonogashira, pp521-549, and pp950-953, hereby incorporated by reference). Structure 30 depicts a representative structure in the presence of the

metal ion and any other necessary ligands; Structure 30 depicts uridine, although as for all the structures herein, any other base may also be used.

Structure 30

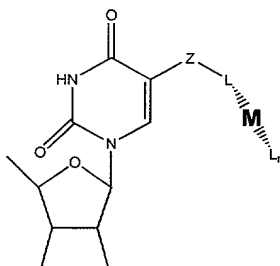


L_a is a ligand, which may include nitrogen, oxygen, sulfur or phosphorus donating ligands or organometallic ligands such as metallocene ligands. Suitable L_a ligands include, but not limited to, phenanthroline, imidazole, bpy and terpy. L_r and M are as defined above. Again, it will be appreciated by those in the art, a linker ("Z") may be included between the nucleoside and the ETM.

Similarly, as for the conductive oligomers, the linkage may be done using a linker, which may utilize an amide linkage (see generally Telser et al., J. Am. Chem. Soc. 111:7221-7226 (1989); Telser et al., J. Am. Chem. Soc. 111:7226-7232 (1989), both of which are expressly incorporated by reference).

These structures are generally depicted below in Structure 31, which again uses uridine as the base, although as above, the other bases may also be used:

Structure 31

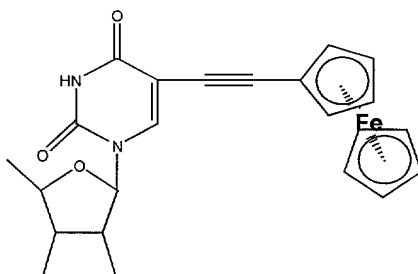


In this embodiment, L is a ligand as defined above, with L_r and M as defined above as well.

Preferably, L is amino, phen, bpy and terpy.

In a preferred embodiment, the ETM attached to a nucleoside is a metallocene; i.e. the L and L_r of Structure 31 are both metallocene ligands, L_m , as described above. Structure 32 depicts a preferred embodiment wherein the metallocene is ferrocene, and the base is uridine, although other bases may be used:

Structure 32

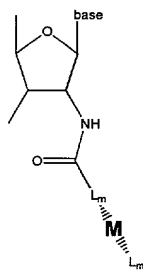


Preliminary data suggest that Structure 32 may cyclize, with the second acetylene carbon atom attacking the carbonyl oxygen, forming a furan-like structure. Preferred metallocenes include ferrocene, cobaltocene and osmiumocene.

In a preferred embodiment, the ETM is attached to a ribose at any position of the ribose-phosphate backbone of the nucleic acid, i.e. either the 5' or 3' terminus or any internal nucleoside. Ribose in this case can include ribose analogs. As is known in the art, nucleosides that are modified at either the 2' or 3' position of the ribose can be made, with nitrogen, oxygen, sulfur and phosphorus-containing modifications possible. Amino-modified and oxygen-modified ribose is preferred. See generally PCT publication WO 95/15971, incorporated herein by reference. These modification groups may be used as a transition metal ligand, or as a chemically functional moiety for attachment of other transition metal ligands and organometallic ligands, or organic electron donor moieties as will be appreciated by those in the art. In this embodiment, a linker such as depicted herein for "Z" may be used as well, or a conductive oligomer between the ribose and the ETM. Preferred embodiments utilize attachment at the 2' or 3' position of the ribose, with the 2' position being preferred. Thus for example, the conductive oligomers depicted in Structure 13, 14 and 15 may be replaced by ETMs; alternatively, the ETMs may be added to the free terminus of the conductive oligomer.

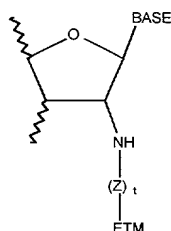
In a preferred embodiment, a metallocene serves as the ETM, and is attached via an amide bond as depicted below in Structure 33. The examples outline the synthesis of a preferred compound when the metallocene is ferrocene.

Structure 33



In a preferred embodiment, amine linkages are used, as is generally depicted in Structure 34.

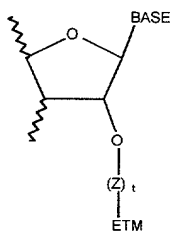
Structure 34



Z is a linker, as defined herein, with 1-16 atoms being preferred, and 2-4 atoms being particularly preferred, and t is either one or zero.

In a preferred embodiment, oxo linkages are used, as is generally depicted in Structure 35.

Structure 35

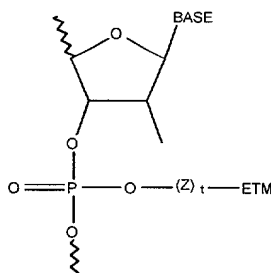


In Structure 35, Z is a linker, as defined herein, and t is either one or zero. Preferred Z linkers include alkyl groups including heteroalkyl groups such as $(CH_2)_n$ and $(CH_2CH_2O)_n$, with n from 1 to 10 being preferred, and n = 1 to 4 being especially preferred, and n=4 being particularly preferred.

Linkages utilizing other heteroatoms are also possible.

In a preferred embodiment, an ETM is attached to a phosphate at any position of the ribose-phosphate backbone of the nucleic acid. This may be done in a variety of ways. In one embodiment, phosphodiester bond analogs such as phosphoramidate or phosphoramidite linkages may be incorporated into a nucleic acid, where the heteroatom (i.e. nitrogen) serves as a transition metal ligand (see PCT publication WO 95/15971, incorporated by reference). Alternatively, the conductive oligomers depicted in Structures 23 and 24 may be replaced by ETMs. In a preferred embodiment, the composition has the structure shown in Structure 36.

Structure 36

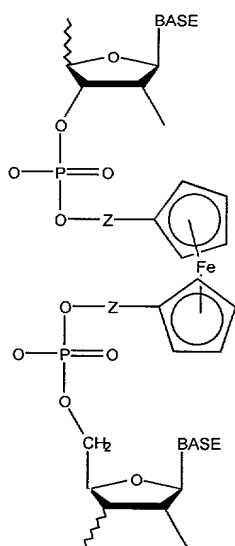


In Structure 361, the ETM is attached via a phosphate linkage, generally through the use of a linker, Z. Preferred Z linkers include alkyl groups, including heteroalkyl groups such as $(CH_2)_n$, $(CH_2CH_2O)_n$, with n from 1 to 10 being preferred, and n = 1 to 4 being especially preferred, and n=4 being particularly preferred.

When the ETM is attached to the base or the backbone of the nucleoside, it is possible to attach the ETMs via “dendrimer” structures, as is more fully outlined below. As is generally depicted in the Figures, alkyl-based linkers can be used to create multiple branching structures comprising one or more ETMs at the terminus of each branch (although internal ETMs can be used as well). Generally, this is done by creating branch points containing multiple hydroxy groups, which optionally can then be used to add additional branch points. The terminal hydroxy groups can then be used in phosphoramidite reactions to add ETMs, as is generally done below for the nucleoside replacement and metallocene polymer reactions. The branch point can be an internal one or a terminal one, and can be a chemical branch point or a nucleoside branch point.

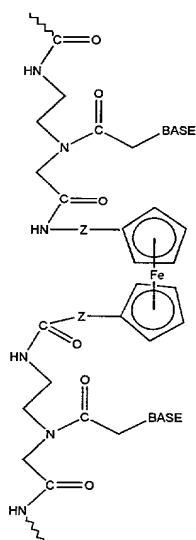
In a preferred embodiment, an ETM such as a metallocene is used as a “nucleoside replacement”, serving as an ETM. For example, the distance between the two cyclopentadiene rings of ferrocene is similar to the orthogononal distance between two bases in a double stranded nucleic acid. Other metallocenes in addition to ferrocene may be used, for example, air stable metallocenes such as those containing cobalt or ruthenium. Thus, metallocene moieties may be incorporated into the backbone of a nucleic acid, as is generally depicted in Structure 37 (nucleic acid with a ribose-phosphate backbone) and Structure 38 (peptide nucleic acid backbone). Structures 37 and 38 depict ferrocene, although as will be appreciated by those in the art, other metallocenes may be used as well. In general, air stable metallocenes are preferred, including metallocenes utilizing ruthenium and cobalt as the metal.

Structure 37



In Structure 37, Z is a linker as defined above, with generally short, alkyl groups, including heteroatoms such as oxygen being preferred. Generally, what is important is the length of the linker, such that minimal perturbations of a double stranded nucleic acid is effected, as is more fully described below. Thus, methylene, ethylene, ethylene glycols, propylene and butylene are all preferred, with ethylene and ethylene glycol being particularly preferred. In addition, each Z linker may be the same or different. Structure 37 depicts a ribose-phosphate backbone, although as will be appreciated by those in the art, nucleic acid analogs may also be used, including ribose analogs and phosphate bond analogs.

Structure 38



In Structure 38, preferred Z groups are as listed above, and again, each Z linker can be the same or different. As above, other nucleic acid analogs may be used as well.

In addition, although the structures and discussion above depicts metallocenes, and particularly ferrocene, this same general idea can be used to add ETMs in addition to metallocenes, as nucleoside replacements or in polymer embodiments, described below. Thus, for example, when the ETM is a transition metal complex other than a metallocene, comprising one, two or three (or more) ligands, the ligands can be functionalized as depicted for the ferrocene to allow the addition of phosphoramidite groups. Particularly preferred in this embodiment are complexes comprising at least two ring (for example, aryl and substituted aryl) ligands, where each of the ligands comprises functional groups for attachment via phosphoramidite chemistry. As will be appreciated by those in the art, this type of reaction, creating polymers of ETMs either as a portion of the backbone of the nucleic acid or as "side groups" of the nucleic acids, to allow amplification of the signals generated herein, can be done with virtually any ETM that can be functionalized to contain the correct chemical groups.

Thus, by inserting a metallocene such as ferrocene (or other ETM) into the backbone of a nucleic acid, nucleic acid analogs are made; that is, the invention provides nucleic acids having a backbone comprising at least one metallocene. This is distinguished from nucleic acids having metallocenes attached to the backbone, i.e. via a ribose, a phosphate, etc. That is, two nucleic acids each made up of a traditional nucleic acid or analog (nucleic acids in this case including a single nucleoside), may be covalently attached to each other via a metallocene. Viewed differently, a metallocene derivative or substituted metallocene is provided, wherein each of the two aromatic rings of the metallocene has a nucleic acid substituent group.

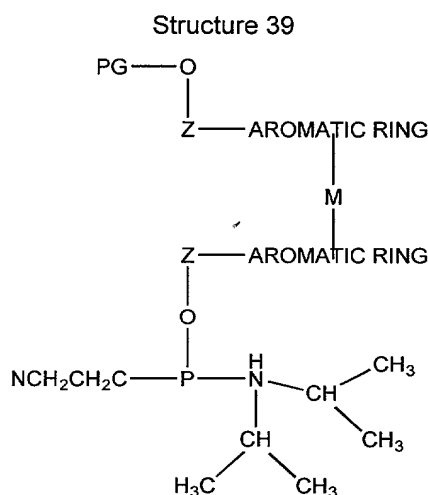
In addition, as is more fully outlined below, it is possible to incorporate more than one metallocene into the backbone, either with nucleotides in between and/or with adjacent metallocenes. When adjacent metallocenes are added to the backbone, this is similar to the process described below as "metallocene polymers"; that is, there are areas of metallocene polymers within the backbone.

In addition to the nucleic acid substituent groups, it is also desirable in some instances to add additional substituent groups to one or both of the aromatic rings of the metallocene (or ETM). For example, as these nucleoside replacements are generally part of probe sequences to be hybridized with a substantially complementary nucleic acid, for example a target sequence or another probe sequence, it is possible to add substituent groups to the metallocene rings to facilitate hydrogen bonding to the base or bases on the opposite strand. These may be added to any position on the metallocene rings. Suitable substituent groups include, but are not limited to, amide groups, amine

groups, carboxylic acids, and alcohols, including substituted alcohols. In addition, these substituent groups can be attached via linkers as well, although in general this is not preferred.

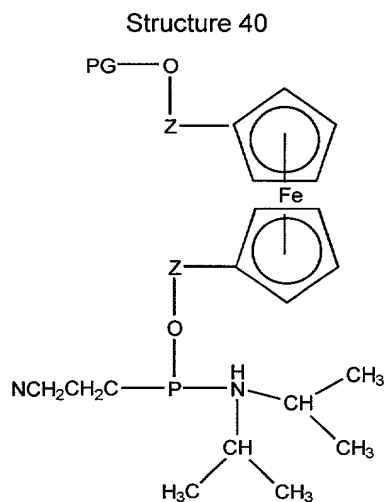
In addition, substituent groups on an ETM, particularly metallocenes such as ferrocene, may be added to alter the redox properties of the ETM. Thus, for example, in some embodiments, as is more fully described below, it may be desirable to have different ETMs attached in different ways (i.e. base or ribose attachment), on different probes, or for different purposes (for example, calibration or as an internal standard). Thus, the addition of substituent groups on the metallocene may allow two different ETMs to be distinguished.

In order to generate these metallocene-backbone nucleic acid analogs, the intermediate components are also provided. Thus, in a preferred embodiment, the invention provides phosphoramidite metallocenes, as generally depicted in Structure 39:



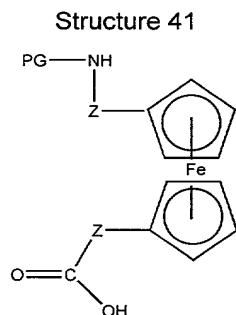
In Structure 39, PG is a protecting group, generally suitable for use in nucleic acid synthesis, with DMT, MMT and TMT all being preferred. The aromatic rings can either be the rings of the metallocene, or aromatic rings of ligands for transition metal complexes or other organic ETMs. The aromatic rings may be the same or different, and may be substituted as discussed herein.

Structure 40 depicts the ferrocene derivative:



These phosphoramidite analogs can be added to standard oligonucleotide syntheses as is known in the art.

Structure 41 depicts the ferrocene peptide nucleic acid (PNA) monomer, that can be added to PNA synthesis as is known in the art and depicted within the Figures and Examples:



In Structure 41, the PG protecting group is suitable for use in peptide nucleic acid synthesis, with MMT, boc and Fmoc being preferred.

These same intermediate compounds can be used to form ETM or metallocene polymers, which are added to the nucleic acids, rather than as backbone replacements, as is more fully described below.

In a preferred embodiment, the ETMs are attached as polymers, for example as metallocene polymers, in a "branched" configuration similar to the "branched DNA" embodiments herein and as outlined in U.S. Patent No. 5,124,246, using modified functionalized nucleotides. The general idea is as follows. A modified phosphoramidite nucleotide is generated that can ultimately contain a free hydroxy group that can be used in the attachment of phosphoramidite ETMs such as metallocenes.

This free hydroxy group could be on the base or the backbone, such as the ribose or the phosphate (although as will be appreciated by those in the art, nucleic acid analogs containing other structures can also be used). The modified nucleotide is incorporated into a nucleic acid, and any hydroxy protecting groups are removed, thus leaving the free hydroxyl. Upon the addition of a phosphoramidite ETM such as a metallocene, as described above in structures 39 and 40, ETMs, such as metallocene ETMs, are added. Additional phosphoramidite ETMs such as metallocenes can be added, to form "ETM polymers", including "metallocene polymers" as depicted herein, particularly for ferrocene. In addition, in some embodiments, it is desirable to increase the solubility of the polymers by adding a "capping" group to the terminal ETM in the polymer, for example a final phosphate group to the metallocene as is generally depicted in Figure 12. Other suitable solubility enhancing "capping" groups will be appreciated by those in the art. It should be noted that these solubility enhancing groups can be added to the polymers in other places, including to the ligand rings, for example on the metallocenes as discussed herein.

A preferred embodiment of this general idea is outlined in the Figures. In this embodiment, the 2' position of a ribose of a phosphoramidite nucleotide is first functionalized to contain a protected hydroxy group, in this case via an oxo-linkage, although any number of linkers can be used, as is generally described herein for Z linkers. The protected modified nucleotide is then incorporated via standard phosphoramidite chemistry into a growing nucleic acid. The protecting group is removed, and the free hydroxy group is used, again using standard phosphoramidite chemistry to add a phosphoramidite metallocene such as ferrocene. A similar reaction is possible for nucleic acid analogs. For example, using peptide nucleic acids and the metallocene monomer shown in Structure 41, peptide nucleic acid structures containing metallocene polymers could be generated.

Thus, the present invention provides recruitment linkers of nucleic acids comprising "branches" of metallocene polymers. Preferred embodiments also utilize metallocene polymers from one to about 50 metallocenes in length, with from about 5 to about 20 being preferred and from about 5 to about 10 being especially preferred.

In a preferred embodiment, the ETMs are attached after the synthesis of the nucleic acids. While the attachment of nucleosides comprising ETMs in either the "comb" structures or "tree" structures work well, there is a limitation on the number of ETMs that can be attached in this manner, due to the limitation of pore size for the solid support during synthesis; large nucleic acids require a large pore size, and thus there is a limit to the number of ETMs, particularly ferrocenes, that can be attached in this manner. Thus, when large amounts of ETMs per nucleic acid are desired, a post-synthesis addition of ETMs may be done. As outlined below, this may be done prior to the assay or during the assay. In addition, while this description relates to the attachment of ETMs, this post-synthesis

addition may be used for the attachment of other detectable labels, such as fluorophores, using a variety of surfaces.

In a preferred embodiment, the addition of the labels occurs prior to the assay. As is outlined in Figure 18, nucleic acids are made that comprise one or more functional groups at the addition position. Preferred functional groups for attachment are amino groups, carboxy groups, maleimide groups, oxo groups and thiol groups, with amino groups and thiol groups being particularly preferred. The addition position will vary with the reaction desired and the nucleic acid used, and can be any position not used for the synthesis of the nucleic acid. For example, when the nucleic acid comprises a ribose-phosphate backbone, the addition position may be the 2' position of the ribose. Alternatively, positions off the base can be used, as is outlined herein for the attachment of ETMs.

In general, the functional group at the addition position can comprise a linker as well, such as an alkyl group, between the first functional group and the nucleic acid, as is generally depicted in Figure 18.

The moiety comprising the label, e.g. the ETM, comprises a functional group as well. As will be appreciated by those in the art, a number of configurations may be used. In one embodiment, the ETM itself comprises a second functional group. Alternatively, and preferred when large numbers of ETMs are to be added, there is a linker or polymer comprising a plurality of ETMs, and the linker or polymer comprises the functional group. For example, as is depicted in Figure 18, a ferrocene polymer attached to an alkyl linker comprising a second functional group can be used.

The two functional groups are then joined, either directly or using a linker. Linkers are known in the art; for example, homo- or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference). The choice of the linker will depend on the functional groups to be joined. For example, when amino and sulfhydryl groups are to be joined, a preferred linker comprises N-(γ-maleimidobutyryloxy) sulfosuccinimide ester (Pierce, supra). Additional preferred linkers include, but are not limited to, alkyl groups (including substituted alkyl groups and alkyl groups containing heteroatom moieties), with short alkyl groups, esters, amide, amine, maleimide groups, epoxy groups and ethylene glycol and derivatives being preferred.

As will be appreciated by those in the art, the order of the additions may vary. For example, the first functional group may be added to the nucleic acid, followed by addition of the linker, followed by addition of the ETM species. Alternatively, the linker may be added to the ETM species and then added to the nucleic acid. Alternatively, the two functional groups are directly attached. Other combinations are possible as well.

In this way, large amounts of ETMs may be added to recruitment linkers.

In a preferred embodiment, the addition of the labels, e.g. ETMs, can actually occur after hybridization, as well. As is shown in Figures 21A and B, functional groups can be incorporated into nucleic acids during synthesis, either directly or through the use of a linker comprising at least one and preferably a plurality of functional groups. The nucleic acids can then be used in the hybridization assay, for example as a label probe, and after hybridization to the capture probe, the labels are added. Again, as above, functional groups are also incorporated into the labels, either directly or as linkers comprising both functional groups and labels. In this way, large amounts of labels, specifically ETMs, can be added to assay complexes.

In addition, when the recruitment linker is nucleic acid, any combination of ETM attachments may be done.

In a preferred embodiment, the recruitment linker is not nucleic acid, and instead may be any sort of linker or polymer. As will be appreciated by those in the art, generally any linker or polymer that can be modified to contain ETMs can be used. In general, the polymers or linkers should be reasonably soluble and contain suitable functional groups for the addition of ETMs.

As used herein, a "recruitment polymer" comprises at least two or three subunits, which are covalently attached. At least some portion of the monomeric subunits contain functional groups for the covalent attachment of ETMs. In some embodiments coupling moieties are used to covalently link the subunits with the ETMs. Preferred functional groups for attachment are amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. As will be appreciated by those in the art, a wide variety of recruitment polymers are possible.

Suitable linkers include, but are not limited to, alkyl linkers (including heteroalkyl (including (poly)ethylene glycol-type structures), substituted alkyl, arylalkyl linkers, etc. As above for the polymers, the linkers will comprise one or more functional groups for the attachment of ETMs, which will be done as will be appreciated by those in the art, for example through the use homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference).

Suitable recruitment polymers include, but are not limited to, functionalized styrenes, such as amino styrene, functionalized dextrans, and polyamino acids. Preferred polymers are polyamino acids (both poly-D-amino acids and poly-L-amino acids), such as polylysine, and polymers containing lysine and other amino acids being particularly preferred. Other suitable polyamino acids are polyglutamic acid,

polyaspartic acid, co-polymers of lysine and glutamic or aspartic acid, co-polymers of lysine with alanine, tyrosine, phenylalanine, serine, tryptophan, and/or proline.

In a preferred embodiment, the recruitment linker comprises a metallocene polymer, as is described above.

The attachment of the recruitment linkers to the first portion of the label probe will depend on the composition of the recruitment linker, as will be appreciated by those in the art. When the recruitment linker is nucleic acid, it is generally formed during the synthesis of the first portion of the label probe, with incorporation of nucleosides containing ETMs as required. Alternatively, the first portion of the label probe and the recruitment linker may be made separately, and then attached. For example, there may be an overlapping section of complementarity, forming a section of double stranded nucleic acid that can then be chemically crosslinked, for example by using psoralen as is known in the art.

When non-nucleic acid recruitment linkers are used, attachment of the linker/polymer of the recruitment linker will be done generally using standard chemical techniques, such as will be appreciated by those in the art. For example, when alkyl-based linkers are used, attachment can be similar to the attachment of insulators to nucleic acids.

In addition, it is possible to have recruitment linkers that are mixtures of nucleic acids and non-nucleic acids, either in a linear form (i.e. nucleic acid segments linked together with alkyl linkers) or in branched forms (nucleic acids with alkyl "branches" that may contain ETMs and may be additionally branched).

In a preferred embodiment, it is the target sequence itself that carries the ETMs, rather than the recruitment linker of a label probe. For example, as is more fully described below, it is possible to enzymatically add triphosphate nucleotides comprising the ETMs of the invention to a growing nucleic acid, for example during a polymerase chain reaction (PCR). As will be recognized by those in the art, while several enzymes have been shown to generally tolerate modified nucleotides, some of the modified nucleotides of the invention, for example the "nucleoside replacement" embodiments and putatively some of the phosphate attachments, may or may not be recognized by the enzymes to allow incorporation into a growing nucleic acid. Therefore, preferred attachments in this embodiment are to the base or ribose of the nucleotide.

Thus, for example, PCR amplification of a target sequence, as is well known in the art, will result in target sequences comprising ETMs, generally randomly incorporated into the sequence. The system

of the invention can then be configured to allow detection using these ETMs, as is generally depicted in Figures 16A, 16B and 16D.

Alternatively, as outlined more fully below, it is possible to enzymatically add nucleotides comprising ETMs to the terminus of a nucleic acid, for example a target nucleic acid. In this embodiment, an effective "recruitment linker" is added to the terminus of the target sequence, that can then be used for detection. Thus the invention provides compositions utilizing electrodes comprising monolayers of conductive oligomers and capture probes, and target sequences that comprises a first portion that is capable of hybridizing to a component of an assay complex, and a second portion that does not hybridize to a component of an assay complex and comprises at least one covalently attached electron transfer moiety. Similarly, methods utilizing these compositions are also provided.

It is also possible to have ETMs connected to probe sequences, i.e. sequences designed to hybridize to complementary sequences. Thus, ETMs may be added to non-recruitment linkers as well. For example, there may be ETMs added to sections of label probes that do hybridize to components of the assay complex, for example the first portion, or to the target sequence as outlined above. These ETMs may be used for electron transfer detection in some embodiments, or they may not, depending on the location and system. For example, in some embodiments, when for example the target sequence containing randomly incorporated ETMs is hybridized directly to the capture probe, as is depicted in Figure 16A, there may be ETMs in the portion hybridizing to the capture probe. If the capture probe is attached to the electrode using a conductive oligomer, these ETMs can be used to detect electron transfer as has been previously described. Alternatively, these ETMs may not be specifically detected.

Similarly, in some embodiments, when the recruitment linker is nucleic acid, it may be desirable in some instances to have some or all of the recruitment linker be double stranded. In one embodiment, there may be a second recruitment linker, substantially complementary to the first recruitment linker, that can hybridize to the first recruitment linker. In a preferred embodiment, the first recruitment linker comprises the covalently attached ETMs. In an alternative embodiment, the second recruitment linker contains the ETMs, and the first recruitment linker does not, and the ETMs are recruited to the surface by hybridization of the second recruitment linker to the first. In yet another embodiment, both the first and second recruitment linkers comprise ETMs. It should be noted, as discussed above, that nucleic acids comprising a large number of ETMs may not hybridize as well, i.e. the T_m may be decreased, depending on the site of attachment and the characteristics of the ETM. Thus, in general, when multiple ETMs are used on hybridizing strands, generally there are less than about 5, with less than about 3 being preferred, or alternatively the ETMs should be spaced sufficiently far apart that the intervening nucleotides can sufficiently hybridize to allow good kinetics.

In one embodiment, non-covalently attached ETMs may be used. In one embodiment, the ETM is a hybridization indicator. Hybridization indicators serve as an ETM that will preferentially associate with double stranded nucleic acid is added, usually reversibly, similar to the method of Millan et al., Anal. Chem. 65:2317-2323 (1993); Millan et al., Anal. Chem. 66:2943-2948 (1994), both of which are hereby expressly incorporated by reference. In this embodiment, increases in the local concentration of ETMs, due to the association of the ETM hybridization indicator with double stranded nucleic acid at the surface, can be monitored using the monolayers comprising the conductive oligomers.

Hybridization indicators include intercalators and minor and/or major groove binding moieties. In a preferred embodiment, intercalators may be used; since intercalation generally only occurs in the presence of double stranded nucleic acid, only in the presence of double stranded nucleic acid will the ETMs concentrate. Intercalating transition metal complex ETMs are known in the art. Similarly, major or minor groove binding moieties, such as methylene blue, may also be used in this embodiment.

Similarly, the systems of the invention may utilize non-covalently attached ETMs, as is generally described in Napier et al., Bioconj. Chem. 8:906 (1997), hereby expressly incorporated by reference. In this embodiment, changes in the redox state of certain molecules as a result of the presence of DNA (i.e. guanine oxidation by ruthenium complexes) can be detected using the SAMs comprising conductive oligomers as well.

Thus, the present invention provides electrodes comprising monolayers comprising conductive oligomers, generally including capture probes, and either target sequences or label probes comprising recruitment linkers containing ETMs. Probes of the present invention are designed to be complementary to a target sequence (either the target sequence of the sample or to other probe sequences, as is described below), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions.

Generally, the nucleic acid compositions of the invention are useful as oligonucleotide probes. As is appreciated by those in the art, the length of the probe will vary with the length of the target sequence and the hybridization and wash conditions. Generally, oligonucleotide probes range from about 8 to about 50 nucleotides, with from about 10 to about 30 being preferred and from about 12 to about 25 being especially preferred. In some cases, very long probes may be used, e.g. 50 to 200-300

nucleotides in length. Thus, in the structures depicted herein, nucleosides may be replaced with nucleic acids.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions; see for example Maniatis et al., *Molecular Cloning: A Laboratory Manual*, 2d Edition, 1989, and *Short Protocols in Molecular Biology*, ed. Ausubel, et al, hereby incorporated by reference. The hybridization conditions may also vary when a non-ionic backbone, i.e. PNA is used, as is known in the art. In addition, cross-linking agents may be added after target binding to cross-link, i.e. covalently attach, the two strands of the hybridization complex.

As will be appreciated by those in the art, the systems of the invention may take on a large number of different configurations, as is generally depicted in the Figures. In general, there are three types of systems that can be used: (1) systems in which the target sequence itself is labeled with ETMs (see Figures 16A, 16B and 16D); (2) systems in which label probes directly hybridize to the target sequences (see Figures 16C and 16H); and (3) systems in which label probes are indirectly hybridized to the target sequences, for example through the use of amplifier probes (see Figures 16E, 16F and 16G).

In all three of these systems, it is preferred, although not required, that the target sequence be immobilized on the electrode surface. This is preferably done using capture probes and optionally one or more capture extender probes. When only capture probes are utilized, it is necessary to have unique capture probes for each target sequence; that is, the surface must be customized to contain unique capture probes. Alternatively, capture extender probes may be used, that allow a "universal" surface, i.e. a surface containing a single type of capture probe that can be used to detect any target sequence. "Capture extender" probes are generally depicted in Figure 14, and have a first portion that will hybridize to all or part of the capture probe, and a second portion that will hybridize to a portion of the target sequence. This then allows the generation of customized soluble probes, which as will be appreciated by those in the art is generally simpler and less costly. As shown herein (e.g. Figure 14C), two capture extender probes may be used. This has generally been done to stabilize assay complexes (for example when the target sequence is large, or when large amplifier probes (particularly branched or dendrimer amplifier probes) are used).

In a preferred embodiment, the nucleic acids are added after the formation of the SAM ((4) above). This may be done in a variety of ways, as will be appreciated by those in the art. In one embodiment, conductive oligomers with terminal functional groups are made, with preferred embodiments utilizing activated carboxylates and isothiocyanates, that will react with primary amines that are put onto the nucleic acid, as is generally depicted in Figure 6 using an activated carboxylate. These two reagents

have the advantage of being stable in aqueous solution, yet react with primary alkylamines. However, the primary aromatic amines and secondary and tertiary amines of the bases should not react, thus allowing site specific addition of nucleic acids to the surface. This allows the spotting of probes (either capture or detection probes, or both) using known methods (ink jet, spotting, etc.) onto the surface.

In addition, there are a number of non-nucleic acid methods that can be used to immobilize a nucleic acid on a surface. For example, binding partner pairs can be utilized; i.e. one binding partner is attached to the terminus of the conductive oligomer, and the other to the end of the nucleic acid. This may also be done without using a nucleic acid capture probe; that is, one binding partner serves as the capture probe and the other is attached to either the target sequence or a capture extender probe. That is, either the target sequence comprises the binding partner, or a capture extender probe that will hybridize to the target sequence comprises the binding partner. Suitable binding partner pairs include, but are not limited to, hapten pairs such as biotin/streptavidin; antigens/antibodies; NTA/histidine tags; etc. In general, smaller binding partners are preferred, such that the electrons can pass from the nucleic acid into the conductive oligomer to allow detection.

In a preferred embodiment, when the target sequence itself is modified to contain a binding partner, the binding partner is attached via a modified nucleotide that can be enzymatically attached to the target sequence, for example during a PCR target amplification step. Alternatively, the binding partner should be easily attached to the target sequence.

Alternatively, a capture extender probe may be utilized that has a nucleic acid portion for hybridization to the target as well as a binding partner (for example, the capture extender probe may comprise a non-nucleic acid portion such as an alkyl linker that is used to attach a binding partner). In this embodiment, it may be desirable to cross-link the double-stranded nucleic acid of the target and capture extender probe for stability, for example using psoralen as is known in the art.

In one embodiment, the target is not bound to the electrode surface using capture probes. In this embodiment, what is important, as for all the assays herein, is that excess label probes be removed prior to detection and that the assay complex (the recruitment linker) be in proximity to the surface. As will be appreciated by those in the art, this may be accomplished in other ways. For example, the assay complex may be present on beads that are added to the electrode comprising the monolayer. The recruitment linkers comprising the ETMs may be placed in proximity to the conductive oligomer surface using techniques well known in the art, including gravity settling of the beads on the surface, electrostatic or magnetic interactions between bead components and the surface, using binding partner attachment as outlined above. Alternatively, after the removal of excess reagents such as

excess label probes, the assay complex may be driven down to the surface, for example by pulsing the system with a voltage sufficient to drive the assay complex to the surface.

However, preferred embodiments utilize assay complexes attached via nucleic acid capture probes.

In a preferred embodiment, the target sequence itself contains the ETMs. As discussed above, this may be done using target sequences that have ETMs incorporated at any number of positions, as outlined above. Representative examples are depicted in Figures 16A, 16B and 16D. In this embodiment, as for the others of the system, the 3'-5' orientation of the probes and targets is chosen to get the ETM-containing structures (i.e. recruitment linkers or target sequences) as close to the surface of the monolayer as possible, and in the correct orientation. This may be done using attachment via insulators or conductive oligomers as is generally shown in the Figures. In addition, as will be appreciated by those in the art, multiple capture probes can be utilized, either in a configuration such as depicted in Figure 16D, wherein the 5'-3' orientation of the capture probes is different, or where "loops" of target form when multiples of capture probes are used.

In a preferred embodiment, the label probes directly hybridize to the target sequences, as is generally depicted in Figure 16C. In these embodiments, the target sequence is preferably, but not required to be, immobilized on the surface using capture probes, including capture extender probes. Label probes are then used to bring the ETMs into proximity of the surface of the monolayer comprising conductive oligomers. In a preferred embodiment, multiple label probes are used; that is, label probes are designed such that the portion that hybridizes to the target sequence (labeled **141** in the figures) can be different for a number of different label probes, such that amplification of the signal occurs, since multiple label probes can bind for every target sequence. Thus, as depicted in the figures, n is an integer of at least one. Depending on the sensitivity desired, the length of the target sequence, the number of ETMs per label probe, etc., preferred ranges of n are from 1 to 50, with from about 1 to about 20 being particularly preferred, and from about 2 to about 5 being especially preferred. In addition, if "generic" label probes are desired, label extender probes can be used as generally described below for use with amplifier probes.

As above, generally in this embodiment the configuration of the system and the label probes are designed to recruit the ETMs as close as possible to the monolayer surface.

In a preferred embodiment, the label probes are hybridized to the target sequence indirectly. That is, the present invention finds use in novel combinations of signal amplification technologies and electron transfer detection on electrodes, which may be particularly useful in sandwich hybridization assays, as generally depicted in Figure 16. In these embodiments, the amplifier probes of the invention are bound

to the target sequence in a sample either directly or indirectly. Since the amplifier probes preferably contain a relatively large number of amplification sequences that are available for binding of label probes, the detectable signal is significantly increased, and allows the detection limits of the target to be significantly improved. These label and amplifier probes, and the detection methods described herein, may be used in essentially any known nucleic acid hybridization formats, such as those in which the target is bound directly to a solid phase or in sandwich hybridization assays in which the target is bound to one or more nucleic acids that are in turn bound to the solid phase.

In general, these embodiments may be described as follows. An amplifier probe is hybridized to the target sequence, either directly (e.g. Figure 16E), or through the use of a label extender probe (e.g. Figure 16F and 16G), which serves to allow “generic” amplifier probes to be made. The target sequence is preferably, but not required to be, immobilized on the electrode using capture probes. Preferably, the amplifier probe contains a multiplicity of amplification sequences, although in some embodiments, as described below, the amplifier probe may contain only a single amplification sequence. The amplifier probe may take on a number of different forms; either a branched conformation, a dendrimer conformation, or a linear “string” of amplification sequences. These amplification sequences are used to form hybridization complexes with label probes, and the ETMs can be detected using the electrode.

Accordingly, the present invention provides assay complexes comprising at least one amplifier probe. By “amplifier probe” or “nucleic acid multimer” or “amplification multimer” or grammatical equivalents herein is meant a nucleic acid probe that is used to facilitate signal amplification. Amplifier probes comprise at least a first single-stranded nucleic acid probe sequence, as defined below, and at least one single-stranded nucleic acid amplification sequence, with a multiplicity of amplification sequences being preferred.

Amplifier probes comprise a first probe sequence that is used, either directly or indirectly, to hybridize to the target sequence. That is, the amplifier probe itself may have a first probe sequence that is substantially complementary to the target sequence (e.g. Figure 16E), or it has a first probe sequence that is substantially complementary to a portion of an additional probe, in this case called a label extender probe, that has a first portion that is substantially complementary to the target sequence (e.g. Figure 16F). In a preferred embodiment, the first probe sequence of the amplifier probe is substantially complementary to the target sequence, as is generally depicted in Figure 16E.

In general, as for all the probes herein, the first probe sequence is of a length sufficient to give specificity and stability. Thus generally, the probe sequences of the invention that are designed to hybridize to another nucleic acid (i.e. probe sequences, amplification sequences, portions or domains

of larger probes) are at least about 5 nucleosides long, with at least about 10 being preferred and at least about 15 being especially preferred.

In a preferred embodiment, as is depicted in Figure 14, the amplifier probes, or any of the other probes of the invention, may form hairpin stem-loop structures in the absence of their target. The length of the stem double-stranded sequence will be selected such that the hairpin structure is not favored in the presence of target. The use of these type of probes, in the systems of the invention or in any nucleic acid detection systems, can result in a significant decrease in non-specific binding and thus an increase in the signal to noise ratio.

Generally, these hairpin structures comprise four components. The first component is a target binding sequence, i.e. a region complementary to the target (which may be the sample target sequence or another probe sequence to which binding is desired), that is about 10 nucleosides long, with about 15 being preferred. The second component is a loop sequence, that can facilitate the formation of nucleic acid loops. Particularly preferred in this regard are repeats of GTC, which has been identified in Fragile X Syndrome as forming turns. (When PNA analogs are used, turns comprising proline residues may be preferred). Generally, from three to five repeats are used, with four to five being preferred. The third component is a self-complementary region, which has a first portion that is complementary to a portion of the target sequence region and a second portion that comprises a first portion of the label probe binding sequence. The fourth component is substantially complementary to a label probe (or other probe, as the case may be). The fourth component further comprises a "sticky end", that is, a portion that does not hybridize to any other portion of the probe, and preferably contains most, if not all, of the ETMs. The general structure is depicted in Figure 14. As will be appreciated by those in the art, the any or all of the probes described herein may be configured to form hairpins in the absence of their targets, including the amplifier, capture, capture extender, label and label extender probes.

In a preferred embodiment, several different amplifier probes are used, each with first probe sequences that will hybridize to a different portion of the target sequence. That is, there is more than one level of amplification; the amplifier probe provides an amplification of signal due to a multiplicity of labelling events, and several different amplifier probes, each with this multiplicity of labels, for each target sequence is used. Thus, preferred embodiments utilize at least two different pools of amplifier probes, each pool having a different probe sequence for hybridization to different portions of the target sequence; the only real limitation on the number of different amplifier probes will be the length of the original target sequence. In addition, it is also possible that the different amplifier probes contain different amplification sequences, although this is generally not preferred.

In a preferred embodiment, the amplifier probe does not hybridize to the sample target sequence directly, but instead hybridizes to a first portion of a label extender probe, as is generally depicted in Figure 16F. This is particularly useful to allow the use of "generic" amplifier probes, that is, amplifier probes that can be used with a variety of different targets. This may be desirable since several of the amplifier probes require special synthesis techniques. Thus, the addition of a relatively short probe as a label extender probe is preferred. Thus, the first probe sequence of the amplifier probe is substantially complementary to a first portion or domain of a first label extender single-stranded nucleic acid probe. The label extender probe also contains a second portion or domain that is substantially complementary to a portion of the target sequence. Both of these portions are preferably at least about 10 to about 50 nucleotides in length, with a range of about 15 to about 30 being preferred. The terms "first" and "second" are not meant to confer an orientation of the sequences with respect to the 5'-3' orientation of the target or probe sequences. For example, assuming a 5'-3' orientation of the complementary target sequence, the first portion may be located either 5' to the second portion, or 3' to the second portion. For convenience herein, the order of probe sequences are generally shown from left to right.

In a preferred embodiment, more than one label extender probe-amplifier probe pair may be used, that is, n is more than 1. That is, a plurality of label extender probes may be used, each with a portion that is substantially complementary to a different portion of the target sequence; this can serve as another level of amplification. Thus, a preferred embodiment utilizes pools of at least two label extender probes, with the upper limit being set by the length of the target sequence.

In a preferred embodiment, more than one label extender probe is used with a single amplifier probe to reduce non-specific binding, as is depicted in Figure 16G and generally outlined in U.S. Patent No. 5,681,697, incorporated by reference herein. In this embodiment, a first portion of the first label extender probe hybridizes to a first portion of the target sequence, and the second portion of the first label extender probe hybridizes to a first probe sequence of the amplifier probe. A first portion of the second label extender probe hybridizes to a second portion of the target sequence, and the second portion of the second label extender probe hybridizes to a second probe sequence of the amplifier probe. These form structures sometimes referred to as "cruciform" structures or configurations, and are generally done to confer stability when large branched or dendrimeric amplifier probes are used.

In addition, as will be appreciated by those in the art, the label extender probes may interact with a preamplifier probe, described below, rather than the amplifier probe directly.

Similarly, as outlined above, a preferred embodiment utilizes several different amplifier probes, each with first probe sequences that will hybridize to a different portion of the label extender probe. In

addition, as outlined above, it is also possible that the different amplifier probes contain different amplification sequences, although this is generally not preferred.

In addition to the first probe sequence, the amplifier probe also comprises at least one amplification sequence. An "amplification sequence" or "amplification segment" or grammatical equivalents herein is meant a sequence that is used, either directly or indirectly, to bind to a first portion of a label probe as is more fully described below. Preferably, the amplifier probe comprises a multiplicity of amplification sequences, with from about 3 to about 1000 being preferred, from about 10 to about 100 being particularly preferred, and about 50 being especially preferred. In some cases, for example when linear amplifier probes are used, from 1 to about 20 is preferred with from about 5 to about 10 being particularly preferred.

The amplification sequences may be linked to each other in a variety of ways, as will be appreciated by those in the art. They may be covalently linked directly to each other, or to intervening sequences or chemical moieties, through nucleic acid linkages such as phosphodiester bonds, PNA bonds, etc., or through interposed linking agents such as amino acid, carbohydrate or polyol bridges, or through other cross-linking agents or binding partners. The site(s) of linkage may be at the ends of a segment, and/or at one or more internal nucleotides in the strand. In a preferred embodiment, the amplification sequences are attached via nucleic acid linkages.

In a preferred embodiment, branched amplifier probes are used, as are generally described in U.S. Patent No. 5,124,246, hereby incorporated by reference. Branched amplifier probes may take on "fork-like" or "comb-like" conformations. "Fork-like" branched amplifier probes generally have three or more oligonucleotide segments emanating from a point of origin to form a branched structure. The point of origin may be another nucleotide segment or a multifunctional molecule to which at least three segments can be covalently or tightly bound. "Comb-like" branched amplifier probes have a linear backbone with a multiplicity of sidechain oligonucleotides extending from the backbone. In either conformation, the pendant segments will normally depend from a modified nucleotide or other organic moiety having the appropriate functional groups for attachment of oligonucleotides. Furthermore, in either conformation, a large number of amplification sequences are available for binding, either directly or indirectly, to detection probes. In general, these structures are made as is known in the art, using modified multifunctional nucleotides, as is described in U.S. Patent Nos. 5,635,352 and 5,124,246, among others.

In a preferred embodiment, dendrimer amplifier probes are used, as are generally described in U.S. Patent No. 5,175,270, hereby expressly incorporated by reference. Dendrimeric amplifier probes have amplification sequences that are attached via hybridization, and thus have portions of double-stranded

nucleic acid as a component of their structure. The outer surface of the dendrimer amplifier probe has a multiplicity of amplification sequences.

In a preferred embodiment, linear amplifier probes are used, that have individual amplification sequences linked end-to-end either directly or with short intervening sequences to form a polymer. As with the other amplifier configurations, there may be additional sequences or moieties between the amplification sequences. In addition, as outlined herein, linear amplification probes may form hairpin stem-loop structures, as is depicted in Figure 14.

In one embodiment, the linear amplifier probe has a single amplification sequence. This may be useful when cycles of hybridization/disassociation occurs, forming a pool of amplifier probe that was hybridized to the target and then removed to allow more probes to bind, or when large numbers of ETMs are used for each label probe. However, in a preferred embodiment, linear amplifier probes comprise a multiplicity of amplification sequences.

In addition, the amplifier probe may be totally linear, totally branched, totally dendrimeric, or any combination thereof.

The amplification sequences of the amplifier probe are used, either directly or indirectly, to bind to a label probe to allow detection. In a preferred embodiment, the amplification sequences of the amplifier probe are substantially complementary to a first portion of a label probe. Alternatively, amplifier extender probes are used, that have a first portion that binds to the amplification sequence and a second portion that binds to the first portion of the label probe.

In addition, the compositions of the invention may include "preamplifier" molecules, which serves a bridging moiety between the label extender molecules and the amplifier probes. In this way, more amplifier and thus more ETMs are ultimately bound to the detection probes. Preamplifier molecules may be either linear or branched, and typically contain in the range of about 30-3000 nucleotides.

The reactions outlined below may be accomplished in a variety of ways, as will be appreciated by those in the art. Components of the reaction may be added simultaneously, or sequentially, in any order, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents may be included in the assays. These include reagents like salts, buffers, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used, depending on the sample preparation methods and purity of the target.

Generally, the methods are as follows. In a preferred embodiment, the target is initially immobilized or attached to the electrode. In one embodiment, this is done by forming a hybridization complex between a capture probe and a portion of the target sequence. A preferred embodiment utilizes capture extender probes; in this embodiment, a hybridization complex is formed between a portion of the target sequence and a first portion of a capture extender probe, and an additional hybridization complex between a second portion of the capture extender probe and a portion of the capture probe. Additional preferred embodiments utilize additional capture probes, thus forming a hybridization complex between a portion of the target sequence and a first portion of a second capture extender probe, and an additional hybridization complex between a second portion of the second capture extender probe and a second portion of the capture probe.

Alternatively, the attachment of the target sequence to the electrode is done simultaneously with the other reactions.

The method proceeds with the introduction of amplifier probes, if utilized. In a preferred embodiment, the amplifier probe comprises a first probe sequence that is substantially complementary to a portion of the target sequence, and at least one amplification sequence.

In one embodiment, the first probe sequence of the amplifier probe is hybridized to the target sequence, and any unhybridized amplifier probe is removed. This will generally be done as is known in the art, and depends on the type of assay. When the target sequence is immobilized on a surface such as an electrode, the removal of excess reagents generally is done via one or more washing steps, as will be appreciated by those in the art. In this embodiment, the target may be immobilized on any solid support. When the target sequence is not immobilized on a surface, the removal of excess reagents such as the probes of the invention may be done by adding beads (i.e. solid support particles) that contain complementary sequences to the probes, such that the excess probes bind to the beads. The beads can then be removed, for example by centrifugation, filtration, the application of magnetic or electrostatic fields, etc.

The reaction mixture is then subjected to conditions (temperature, high salt, changes in pH, etc.) under which the amplifier probe disassociates from the target sequence, and the amplifier probe is collected. The amplifier probe may then be added to an electrode comprising capture probes for the amplifier probes, label probes added, and detection is achieved.

In a preferred embodiment, a larger pool of probe is generated by adding more amplifier probe to the target sequence and the hybridization/disassociation reactions are repeated, to generate a larger pool

of amplifier probe. This pool of amplifier probe is then added to an electrode comprising amplifier capture probes, label probes added, and detection proceeds.

In this embodiment, it is preferred that the target sequence be immobilized on a solid support, including an electrode, using the methods described herein; although as will be appreciated by those in the art, alternate solid support attachment technologies may be used, such as attachment to glass, polymers, etc. It is possible to do the reaction on one solid support and then add the pooled amplifier probe to an electrode for detection.

In a preferred embodiment, the amplifier probe comprises a multiplicity of amplification sequences.

In one embodiment, the first probe sequence of the amplifier probe is hybridized to the target sequence, and any unhybridized amplifier probe is removed. Again, preferred embodiments utilize immobilized target sequences, wherein the target sequences are immobilized by hybridization with capture probes that are attached to the electrode, or hybridization to capture extender probes that in turn hybridize with immobilized capture probes as is described herein. Generally, in these embodiments, the capture probes and the detection probes are immobilized on the electrode, generally at the same "address".

In a preferred embodiment, the first probe sequence of the amplifier probe is hybridized to a first portion of at least one label extender probe, and a second portion of the label extender probe is hybridized to a portion of the target sequence. Other preferred embodiments utilize more than one label extender probe.

In a preferred embodiment, the amplification sequences of the amplifier probe are used directly for detection, by hybridizing at least one label probe sequence.

The invention thus provides assay complexes that minimally comprise a target sequence and a label probe. "Assay complex" herein is meant the collection of hybridization complexes comprising nucleic acids, including probes and targets, that contains at least one ETM and thus allows detection. The composition of the assay complex depends on the use of the different probe component outlined herein. Thus, the assay complex comprises the capture probe and the target sequence. The assay complexes may also include label probes, capture extender probes, label extender probes, and amplifier probes, as outlined herein, depending on the configuration used.

The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step

parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc. Stringency may also include the use of an electrophoretic step to drive non-specific (i.e. low stringency) materials away from the detection electrode, just as electrophoresis can be used to bind the target analytes to their binding ligands, as is described in U.S.S.N. 09.134,058, hereby expressly incorporated by reference.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions; for example, when an initial hybridization step is done between the target sequence and the label extender and capture extender probes. Running this step at conditions which favor specific binding can allow the reduction of non-specific binding.

In a preferred embodiment, when all of the components outlined herein are used, a preferred method is as follows. Single-stranded target sequence is incubated under hybridization conditions with the capture extender probes and the label extender probes. A preferred embodiment does this reaction in the presence of the electrode with immobilized capture probes, although this may also be done in two steps, with the initial incubation and the subsequent addition to the electrode. Excess reagents are washed off, and amplifier probes are then added. If preamplifier probes are used, they may be added either prior to the amplifier probes or simultaneously with the amplifier probes. Excess reagents are washed off, and label probes are then added. Excess reagents are washed off, and detection proceeds as outlined below.

In one embodiment, a number of capture probes (or capture probes and capture extender probes) that are each substantially complementary to a different portion of the target sequence are used.

Again, as outlined herein, when amplifier probes are used, the system is generally configured such that upon label probe binding, the recruitment linkers comprising the ETMs are placed in proximity to the monolayer surface. Thus for example, when the ETMs are attached via "dendrimer" type structures as outlined herein, the length of the linkers from the nucleic acid point of attachment to the ETMs may vary, particularly with the length of the capture probe when capture extender probes are used. That is, longer capture probes, with capture extenders, can result in the target sequences being "held" further away from the surface than for shorter capture probes. Adding extra linking sequences between the probe nucleic acid and the ETMs can result in the ETMs being spatially closer to the surface, giving better results.

In addition, if desirable, nucleic acids utilized in the invention may also be ligated together prior to detection, if applicable, by using standard molecular biology techniques such as the use of a ligase. Similarly, if desirable for stability, cross-linking agents may be added to hold the structures stable.

The compositions of the invention are generally synthesized as outlined below, generally utilizing techniques well known in the art. As will be appreciated by those in the art, many of the techniques outlined below are directed to nucleic acids containing a ribose-phosphate backbone. However, as outlined above, many alternate nucleic acid analogs may be utilized, some of which may not contain either ribose or phosphate in the backbone. In these embodiments, for attachment at positions other than the base, attachment is done as will be appreciated by those in the art, depending on the backbone. Thus, for example, attachment can be made at the carbon atoms of the PNA backbone, as is described below, or at either terminus of the PNA.

The compositions may be made in several ways. A preferred method first synthesizes a conductive oligomer attached to a nucleoside, with addition of additional nucleosides to form the capture probe followed by attachment to the electrode. Alternatively, the whole capture probe may be made and then the completed conductive oligomer added, followed by attachment to the electrode. Alternatively, a monolayer of conductive oligomer (some of which have functional groups for attachment of capture probes) is attached to the electrode first, followed by attachment of the capture probe. The latter two methods may be preferred when conductive oligomers are used which are not stable in the solvents and under the conditions used in traditional nucleic acid synthesis.

In a preferred embodiment, the compositions of the invention are made by first forming the conductive oligomer covalently attached to the nucleoside, followed by the addition of additional nucleosides to form a capture probe nucleic acid, with the last step comprising the addition of the conductive oligomer to the electrode.

The attachment of the conductive oligomer to the nucleoside may be done in several ways. In a preferred embodiment, all or part of the conductive oligomer is synthesized first (generally with a functional group on the end for attachment to the electrode), which is then attached to the nucleoside. Additional nucleosides are then added as required, with the last step generally being attachment to the electrode. Alternatively, oligomer units are added one at a time to the nucleoside, with addition of additional nucleosides and attachment to the electrode. A number of representative syntheses are shown in the Figures of PCT US97/20014, expressly incorporated herein by reference.

The conductive oligomer is then attached to a nucleoside that may contain one (or more) of the oligomer units, attached as depicted herein.

In a preferred embodiment, attachment is to a ribose of the ribose-phosphate backbone. Thus, attachment via amide and amine linkages are possible (see Figures 1 and 2 of CPT US97/20014). In a preferred embodiment, there is at least a methylene group or other short aliphatic alkyl groups (as a Z group) between the nitrogen attached to the ribose and the aromatic ring of the conductive oligomer. A representative synthesis is shown in Figure 16 of PCT US97/20014.

Alternatively, attachment is via a phosphate of the ribose-phosphate backbone. Examples of two synthetic schemes are shown in Figure 4 and Figure 5 of PCT US97/20014. Although both Figures show attachment at the 3' position of the ribose, attachment can also be made via the 2' position. In Figure 5, Z is an ethylene linker, although other linkers may be used as well, as will be appreciated by those in the art.

In a preferred embodiment, attachment is via the base. A general scheme is depicted in Figure 3 of PCT US97/20014, using uridine as the nucleoside and a phenylene-acetylene conductive oligomer. As will be appreciated in the art, amide linkages are also possible, using techniques well known in the art. In a preferred embodiment, protecting groups may be added to the base prior to addition of the conductive oligomers, as is generally outlined in Figures 10 and 11 of PCT US97/20014. In addition, the palladium cross-coupling reactions may be altered to prevent dimerization problems; i.e. two conductive oligomers dimerizing, rather than coupling to the base.

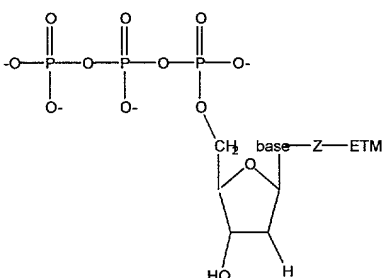
Alternatively, attachment to the base may be done by making the nucleoside with one unit of the oligomer, followed by the addition of others.

Once the modified nucleosides are prepared, protected and activated, prior to attachment to the electrode, they may be incorporated into a growing oligonucleotide by standard synthetic techniques (Gait, *Oligonucleotide Synthesis: A Practical Approach*, IRL Press, Oxford, UK 1984; Eckstein) in several ways.

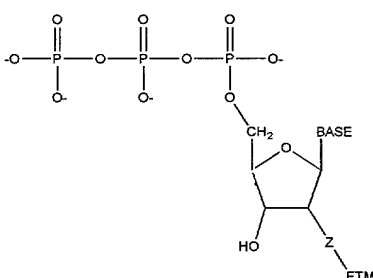
In preferred embodiments, one or more modified nucleosides are converted to the triphosphate form and incorporated into a growing oligonucleotide chain by using standard molecular biology techniques such as with the use of the enzyme DNA polymerase I, T4 DNA polymerase, T7 DNA polymerase, Taq DNA polymerase, reverse transcriptase, and RNA polymerases. For the incorporation of a 3' modified nucleoside to a nucleic acid, terminal deoxynucleotidyltransferase may be used. (Ratcliff, *Terminal deoxynucleotidyltransferase*. In *The Enzymes*, Vol 14A. P.D. Boyer ed. pp 105-118. Academic Press, San Diego, CA. 1981). Thus, the present invention provides deoxyribonucleoside triphosphates comprising a covalently attached ETM. Preferred embodiments utilize ETM attachment

to the base or the backbone, such as the ribose (preferably in the 2' position), as is generally depicted below in Structures 42 and 43:

Structure 42



Structure 43



Thus, in some embodiments, it may be possible to generate the nucleic acids comprising ETMs in situ. For example, a target sequence can hybridize to a capture probe (for example on the surface) in such a way that the terminus of the target sequence is exposed, i.e. unhybridized. The addition of enzyme and triphosphate nucleotides labelled with ETMs allows the in situ creation of the label. Similarly, using labeled nucleotides recognized by polymerases can allow simultaneous PCR and detection; that is, the target sequences are generated in situ.

In a preferred embodiment, the modified nucleoside is converted to the phosphoramidite or H-phosphonate form, which are then used in solid-phase or solution syntheses of oligonucleotides. In this way the modified nucleoside, either for attachment at the ribose (i.e. amino- or thiol-modified nucleosides) or the base, is incorporated into the oligonucleotide at either an internal position or the 5' terminus. This is generally done in one of two ways. First, the 5' position of the ribose is protected with 4',4-dimethoxytrityl (DMT) followed by reaction with either 2-cyanoethoxy-bis-diisopropylaminophosphine in the presence of diisopropylammonium tetrazolide, or by reaction with chlorodiisopropylamino 2'-cyanoethoxyphosphine, to give the phosphoramidite as is known in the art; although other techniques may be used as will be appreciated by those in the art. See Gait, *supra*; Caruthers, *Science* 230:281 (1985), both of which are expressly incorporated herein by reference.

For attachment of a group to the 3' terminus, a preferred method utilizes the attachment of the modified nucleoside (or the nucleoside replacement) to controlled pore glass (CPG) or other oligomeric supports. In this embodiment, the modified nucleoside is protected at the 5' end with DMT, and then reacted with succinic anhydride with activation. The resulting succinyl compound is attached to CPG or other oligomeric supports as is known in the art. Further phosphoramidite nucleosides are added, either modified or not, to the 5' end after deprotection. Thus, the present invention provides conductive oligomers or insulators covalently attached to nucleosides attached to solid oligomeric supports such as CPG, and phosphoramidite derivatives of the nucleosides of the invention.

The invention further provides methods of making label probes with recruitment linkers comprising ETMs. These synthetic reactions will depend on the character of the recruitment linker and the method of attachment of the ETM, as will be appreciated by those in the art. For nucleic acid recruitment linkers, the label probes are generally made as outlined herein with the incorporation of ETMs at one or more positions. When a transition metal complex is used as the ETM, synthesis may occur in several ways. In a preferred embodiment, the ligand(s) are added to a nucleoside, followed by the transition metal ion, and then the nucleoside with the transition metal complex attached is added to an oligonucleotide, i.e. by addition to the nucleic acid synthesizer. Alternatively, the ligand(s) may be attached, followed by incorporation into a growing oligonucleotide chain, followed by the addition of the metal ion.

In a preferred embodiment, ETMs are attached to a ribose of the ribose-phosphate backbone. This is generally done as is outlined herein for conductive oligomers, as described herein, and in PCT publication WO 95/15971, using amino-modified or oxo-modified nucleosides, at either the 2' or 3' position of the ribose. The amino group may then be used either as a ligand, for example as a transition metal ligand for attachment of the metal ion, or as a chemically functional group that can be used for attachment of other ligands or organic ETMs, for example via amide linkages, as will be appreciated by those in the art. For example, the examples describe the synthesis of nucleosides with a variety of ETMs attached via the ribose.

In a preferred embodiment, ETMs are attached to a phosphate of the ribose-phosphate backbone. As outlined herein, this may be done using phosphodiester analogs such as phosphoramidite bonds, see generally PCT publication WO 95/15971, or can be done in a similar manner to that depicted in Figures 4 and 5 of PCT US97/20014, where the conductive oligomer is replaced by a transition metal ligand or complex or an organic ETM, as well as is outlined in the Examples.

Attachment to alternate backbones, for example peptide nucleic acids or alternate phosphate linkages will be done as will be appreciated by those in the art.

In a preferred embodiment, ETMs are attached to a base of the nucleoside. This may be done in a variety of ways. In one embodiment, amino groups of the base, either naturally occurring or added as is described herein (see the figures, for example), are used either as ligands for transition metal complexes or as a chemically functional group that can be used to add other ligands, for example via an amide linkage, or organic ETMs. This is done as will be appreciated by those in the art. Alternatively, nucleosides containing halogen atoms attached to the heterocyclic ring are commercially available. Acetylene linked ligands may be added using the halogenated bases, as is generally known; see for example, Tzalis et al., *Tetrahedron Lett.* 36(34):6017-6020 (1995); Tzalis et al., *Tetrahedron Lett.* 36(2):3489-3490 (1995); and Tzalis et al., *Chem. Communications* (in press) 1996, all of which are hereby expressly incorporated by reference. See also the figures and the examples, which describes the synthesis of metallocenes (in this case, ferrocene) attached via acetylene linkages to the bases.

In one embodiment, the nucleosides are made with transition metal ligands, incorporated into a nucleic acid, and then the transition metal ion and any remaining necessary ligands are added as is known in the art. In an alternative embodiment, the transition metal ion and additional ligands are added prior to incorporation into the nucleic acid.

Once the nucleic acids of the invention are made, with a covalently attached attachment linker (i.e. either an insulator or a conductive oligomer), the attachment linker is attached to the electrode. The method will vary depending on the type of electrode used. As is described herein, the attachment linkers are generally made with a terminal "A" linker to facilitate attachment to the electrode. For the purposes of this application, a sulfur-gold attachment is considered a covalent attachment.

In a preferred embodiment, conductive oligomers, insulators, and attachment linkers are covalently attached via sulfur linkages to the electrode. However, surprisingly, traditional protecting groups for use of attaching molecules to gold electrodes are generally not ideal for use in both synthesis of the compositions described herein and inclusion in oligonucleotide synthetic reactions. Accordingly, the present invention provides novel methods for the attachment of conductive oligomers to gold electrodes, utilizing unusual protecting groups, including ethylpyridine, and trimethylsilylethyl as is depicted in the Figures. However, as will be appreciated by those in the art, when the conductive oligomers do not contain nucleic acids, traditional protecting groups such as acetyl groups and others may be used. See Greene et al., *supra*.

This may be done in several ways. In a preferred embodiment, the subunit of the conductive oligomer which contains the sulfur atom for attachment to the electrode is protected with an ethyl-pyridine or trimethylsilylethyl group. For the former, this is generally done by contacting the subunit containing the

sulfur atom (preferably in the form of a sulfhydryl) with a vinyl pyridine group or vinyl trimethylsilylethyl group under conditions whereby an ethylpyridine group or trimethylsilylethyl group is added to the sulfur atom.

This subunit also generally contains a functional moiety for attachment of additional subunits, and thus additional subunits are attached to form the conductive oligomer. The conductive oligomer is then attached to a nucleoside, and additional nucleosides attached. The protecting group is then removed and the sulfur-gold covalent attachment is made. Alternatively, all or part of the conductive oligomer is made, and then either a subunit containing a protected sulfur atom is added, or a sulfur atom is added and then protected. The conductive oligomer is then attached to a nucleoside, and additional nucleosides attached. Alternatively, the conductive oligomer attached to a nucleic acid is made, and then either a subunit containing a protected sulfur atom is added, or a sulfur atom is added and then protected. Alternatively, the ethyl pyridine protecting group may be used as above, but removed after one or more steps and replaced with a standard protecting group like a disulfide. Thus, the ethyl pyridine or trimethylsilylethyl group may serve as the protecting group for some of the synthetic reactions, and then removed and replaced with a traditional protecting group.

By "subunit" of a conductive polymer herein is meant at least the moiety of the conductive oligomer to which the sulfur atom is attached, although additional atoms may be present, including either functional groups which allow the addition of additional components of the conductive oligomer, or additional components of the conductive oligomer. Thus, for example, when Structure 1 oligomers are used, a subunit comprises at least the first Y group.

A preferred method comprises 1) adding an ethyl pyridine or trimethylsilylethyl protecting group to a sulfur atom attached to a first subunit of a conductive oligomer, generally done by adding a vinyl pyridine or trimethylsilylethyl group to a sulfhydryl; 2) adding additional subunits to form the conductive oligomer; 3) adding at least a first nucleoside to the conductive oligomer; 4) adding additional nucleosides to the first nucleoside to form a nucleic acid; 5) attaching the conductive oligomer to the gold electrode. This may also be done in the absence of nucleosides, as is described in the Examples.

The above method may also be used to attach insulator molecules to a gold electrode.

In a preferred embodiment, a monolayer comprising conductive oligomers (and optionally insulators) is added to the electrode. Generally, the chemistry of addition is similar to or the same as the addition of conductive oligomers to the electrode, i.e. using a sulfur atom for attachment to a gold electrode, etc. Compositions comprising monolayers in addition to the conductive oligomers covalently attached to

nucleic acids may be made in at least one of five ways: (1) addition of the monolayer, followed by subsequent addition of the attachment linker-nucleic acid complex; (2) addition of the attachment linker-nucleic acid complex followed by addition of the monolayer; (3) simultaneous addition of the monolayer and attachment linker-nucleic acid complex; (4) formation of a monolayer (using any of 1, 2 or 3) which includes attachment linkers which terminate in a functional moiety suitable for attachment of a completed nucleic acid; or (5) formation of a monolayer which includes attachment linkers which terminate in a functional moiety suitable for nucleic acid synthesis, i.e. the nucleic acid is synthesized on the surface of the monolayer as is known in the art. Such suitable functional moieties include, but are not limited to, nucleosides, amino groups, carboxyl groups, protected sulfur moieties, or hydroxyl groups for phosphoramidite additions. The examples describe the formation of a monolayer on a gold electrode using the preferred method (1).

In a preferred embodiment, the nucleic acid is a peptide nucleic acid or analog. In this embodiment, the invention provides peptide nucleic acids with at least one covalently attached ETM or attachment linker. In a preferred embodiment, these moieties are covalently attached to an monomeric subunit of the PNA. By "monomeric subunit of PNA" herein is meant the $\text{-NH-CH}_2\text{CH}_2\text{-N(COCH}_2\text{-Base)-CH}_2\text{-CO-}$ monomer, or derivatives (herein included within the definition of "nucleoside") of PNA. For example, the number of carbon atoms in the PNA backbone may be altered; see generally Nielsen et al., Chem. Soc. Rev. 1997 page 73, which discloses a number of PNA derivatives, herein expressly incorporated by reference. Similarly, the amide bond linking the base to the backbone may be altered; phosphoramidate and sulfuramidate bonds may be used. Alternatively, the moieties are attached to an internal monomeric subunit. By "internal" herein is meant that the monomeric subunit is not either the N-terminal monomeric subunit or the C-terminal monomeric subunit. In this embodiment, the moieties can be attached either to a base or to the backbone of the monomeric subunit. Attachment to the base is done as outlined herein or known in the literature. In general, the moieties are added to a base which is then incorporated into a PNA as outlined herein. The base may be either protected, as required for incorporation into the PNA synthetic reaction, or derivatized, to allow incorporation, either prior to the addition of the chemical substituent or afterwards. Protection and derivatization of the bases is shown in Figures 24-27 of PCT US97/20014. The bases can then be incorporated into monomeric subunits as shown in Figure 28 of PCT US97/20014. Figures 29 and 30 of PCT US97/20014 depict two different chemical substituents, an ETM and a conductive oligomer, attached at a base. Figure 29 depicts a representative synthesis of a PNA monomeric subunit with a ferrocene attached to a uracil base. Figure 30 depicts the synthesis of a three unit conductive oligomer attached to a uracil base.

In a preferred embodiment, the moieties are covalently attached to the backbone of the PNA monomer. The attachment is generally to one of the unsubstituted carbon atoms of the monomeric

subunit, preferably the α -carbon of the backbone, as is depicted in Figures 31 and 32, although attachment at either of the carbon 1 or 2 positions, or the α -carbon of the amide bond linking the base to the backbone may be done. In the case of PNA analogs, other carbons or atoms may be substituted as well. In a preferred embodiment, moieties are added at the α -carbon atoms, either to a terminal monomeric subunit or an internal one.

In this embodiment, a modified monomeric subunit is synthesized with an ETM or an attachment linker, or a functional group for its attachment, and then the base is added and the modified monomer can be incorporated into a growing PNA chain. Figure 31 of PCT US97/20014 depicts the synthesis of a conductive oligomer covalently attached to the backbone of a PNA monomeric subunit, and Figure 32 of PCT US97/20014 depicts the synthesis of a ferrocene attached to the backbone of a monomeric subunit.

Once generated, the monomeric subunits with covalently attached moieties are incorporated into a PNA using the techniques outlined in Will et al., *Tetrahedron* 51(44):12069-12082 (1995), and Vanderlaan et al., *Tett. Let.* 38:2249-2252 (1997), both of which are hereby expressly incorporated in their entirety. These procedures allow the addition of chemical substituents to peptide nucleic acids without destroying the chemical substituents.

As will be appreciated by those in the art, electrodes may be made that have any combination of nucleic acids, conductive oligomers and insulators.

The compositions of the invention may additionally contain one or more labels at any position. By "label" herein is meant an element (e.g. an isotope) or chemical compound that is attached to enable the detection of the compound. Preferred labels are radioactive isotopic labels, and colored or fluorescent dyes. The labels may be incorporated into the compound at any position. In addition, the compositions of the invention may also contain other moieties such as cross-linking agents to facilitate cross-linking of the target-probe complex. See for example, Lukhtanov et al., *Nucl. Acids. Res.* 24(4):683 (1996) and Tabone et al., *Biochem.* 33:375 (1994), both of which are expressly incorporated by reference.

Without being bound by theory, it appears that while the presence of a SAM on the electrode greatly facilitates the reduction of non-specific binding, particularly of electroactive species that can interfere with the assay, as is discussed above, electron transfer is promoted when the ETM is able to penetrate the monolayer to gain better access to the electrode, or if the monolayer is not present. That is, "shorter" monolayers can give rise to better signals.

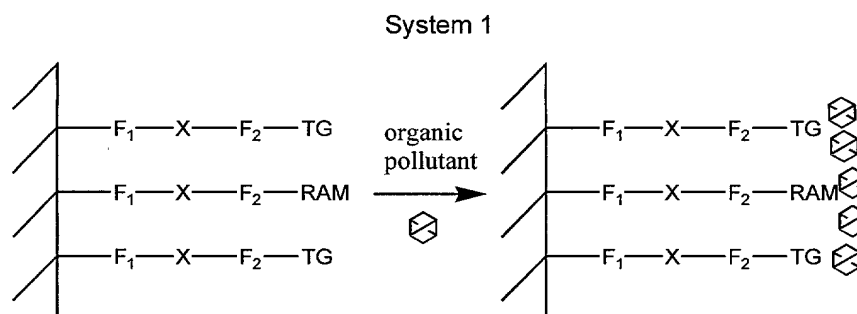
Thus, in a preferred embodiment, the methods of the present invention comprise forming a first monolayer, capturing the target analyte, and then removing or replacing the monolayer with a different type of monolayer that allows better access of the ETM to the electrode. This effectively gives the benefit of having a SAM (reduction of non-specific binding) yet allows good access of the ETMs to the electrode to facilitate signalling.

Accordingly, in this embodiment, the methods comprise adding the target analyte to an electrode that has a first SAM forming species comprising a capture binding ligand and at least a second SAM forming species. The second SAM forming species can comprise insulators, for example on rough surfaces, or a mixture of insulators and EFS. The capture binding ligand and the target analyte form a binding complex (termed a hybridization complex when the capture binding ligand and the target analyte are nucleic acids; as outlined herein, this hybridization complex may comprise additional nucleic acids, such as capture extender probes, etc.). This binding complex may comprise ETMs, in which case it is also an assay complex, or the ETMs may be added after the replacement step, in the form of solution binding ligands (termed label probes in the case of nucleic acids).

A third SAM forming species is then added that replaces the second SAM forming species. Interestingly, it appears that “short” monolayer forming species, such as alkyl thiol species of C2 to C6, will replace non-capture binding ligand monolayer forming species; that is, capture binding ligand species are preferentially retained, while other SAM forming species are displaced. Thus, this displacement step does not appear to significantly remove the binding complexes from the surface. However, significant increases in signal from the ETMs can be seen. Furthermore, after displacement, particularly with C2 species, even charged hydrophilic ETMs can signal, thus inferring that the electrode is not significantly protected.

An assay complex is then formed; that is, if not already present, ETMs are added, in the form of solution binding ligands, such that the assay complex comprises the target analyte, the capture binding ligand, and at least one electron transfer moiety (ETM). Detection then proceeds as outlined below.

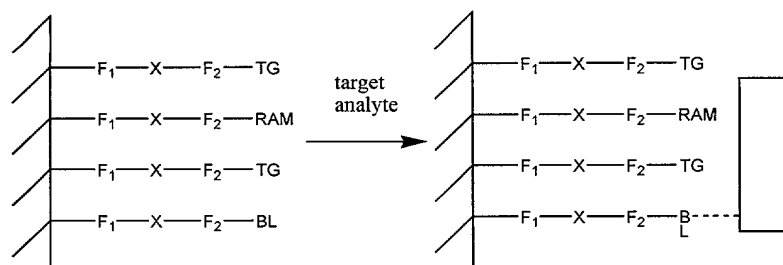
In addition to nucleic acids, other types of target analytes may be detected. In a preferred embodiment, the system is used to detect pollutants, such as organic pollutants, as is depicted below in System 1:



In System 1, as is described below, the hatched marks indicate an electrode, and there is preferably a monolayer on the surface. F_1 is a linkage that allows the covalent attachment of the electrode and the conductive oligomer or insulator, including bonds, atoms or linkers such as is described herein, for example as "A", defined below. F_2 is a linkage that allows the covalent attachment of the conductive oligomer or insulator, and may be a bond, an atom or a linkage as is herein described. F_2 may be part of the conductive oligomer, part of the insulator, part of the terminal group, part of the redox active complex or component, or exogenous to both, for example, as defined herein for "Z". X is a spacer (conductive oligomer, passivation agent or insulator, as required). RAM is a redox active molecule, sometimes referred to herein as an ETM. TG is a terminal group, which may be chosen to influence the association of the target pollutant, such as an organic pollutant. Thus for example in this embodiment TG may be hydrophobic. The association of the pollutant on the surface will affect the local environment of the RAM, for example potentially by changing the E_0 of the RAM or the solvent reorganization energy, and thus results in a change in the faradaic impedance of the system in the presence of the analyte. The association in this case is not specific for a particular analyte.

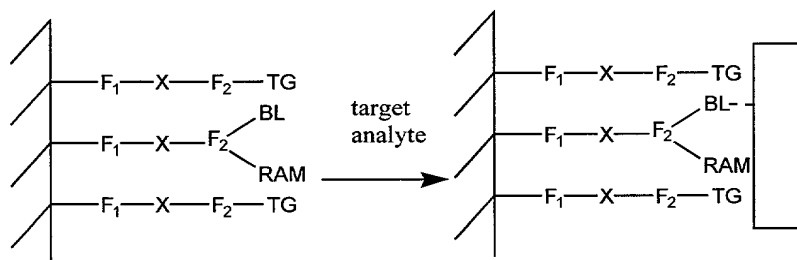
Systems 2, 3, 4 and 5 depict a similar situation except that a specific interaction is exploited. Thus, the target analyte will bind to the binding ligand specifically, and is generally large as compared to the binding ligand and RAM. Upon binding, the local environment of the RAM is affected, for example potentially by changing the E_0 of the RAM or the solvent reorganization energy, and thus results in a change in the faradaic impedance of the system in the presence of the analyte. The target analyte in these cases could be protein, a cell, etc. In addition, any or all of these systems may be used with co-redoxants, as described below. Upon binding of the target analyte, the access of the co-redoxant to the RAM is restricted, thus resulting in either a different signal or a loss in signal, or both. In addition, as for all the systems depicted herein, the order or proximity of the individual molecules of the monolayer is not determinative.

System 2

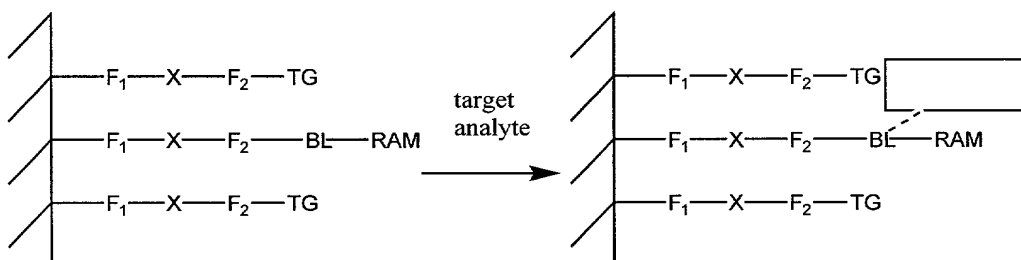


In System 2, there may be more than one RAM per binding ligand (BL); that is, the ratio of RAM to BL on the surface (depending on the relative size of the target analyte) may range from 1:1 to over 100:1. This allows an amplification of signal, in that more than one RAM is used to detect a single target analyte.

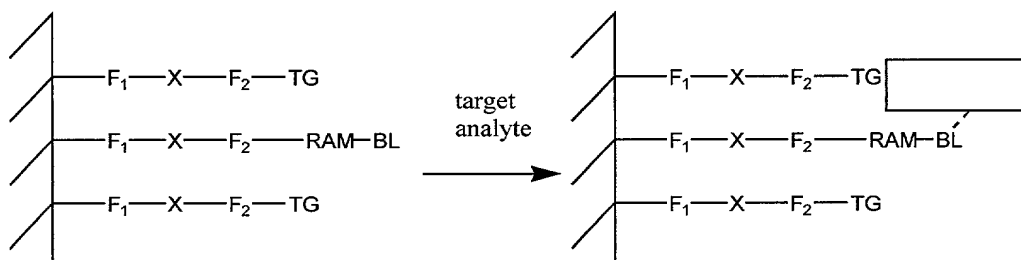
System 3



System 4

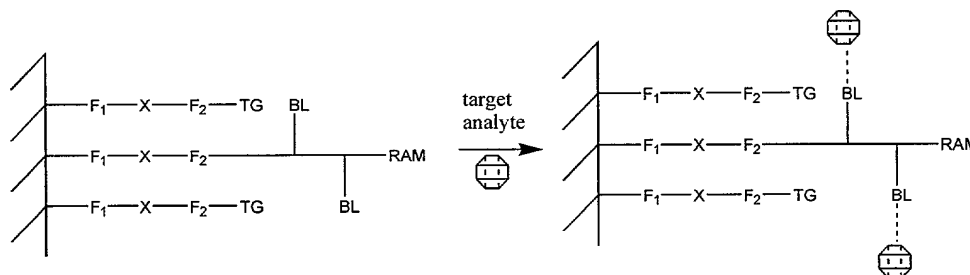


System 5



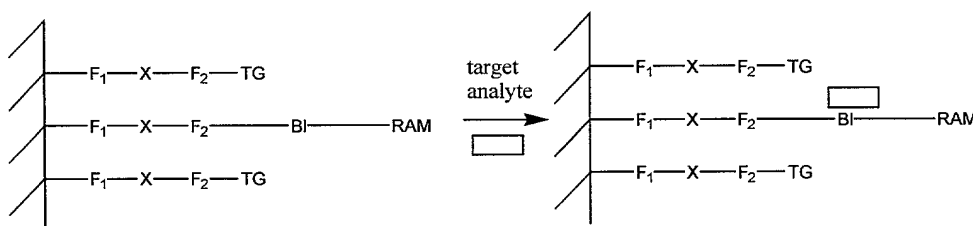
System 6 depicts a system in which binding of a target analyte theoretically affects the H_{AB} between the RAM and the electrode:

System 6



System 7 depicts a similar situation, except that the binding ligand is inherent in the attachment of the RAM to the electrode; for example, it may be a peptide or nucleic acid to which the analyte binds:

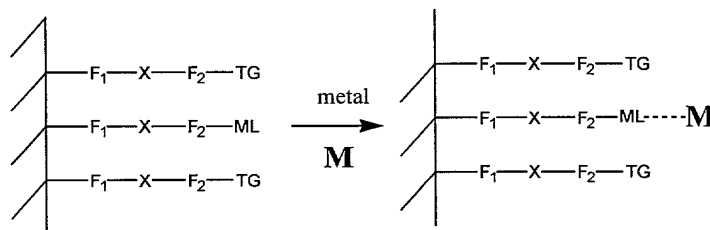
System 7



System 8 depicts a situation in which the analyte also serves as the redox active molecule; this is particularly useful in the detection of metal ions, for example heavy metal ions, which are toxic.

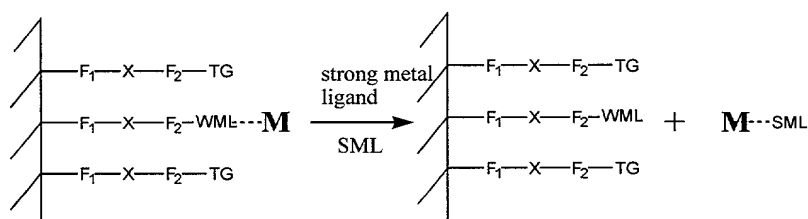
System 8 depicts a metal ion, M , and a metal ligand, ML , although as will be appreciated by those in the art, it is quite possible to have the analyte in this case be a metalloprotein, with a BL, etc. As will be appreciated by those in the art, System 8 is particularly useful in the detection of different metal ions, using an array of different ligands; preferential binding of one metal over another would result in a panel of results that can be correlated to metal ligand binding. Moreover, different metals may have different E_0 s and thus give different signals.

System 8



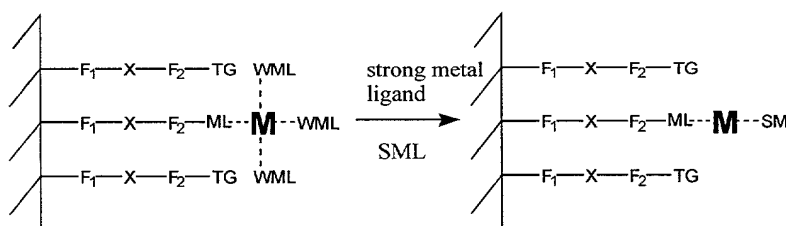
System 9 depicts a competitive-type assay which relies on a decrease in signal for detection. In this case, the target analyte is a ligand, for example carbon monoxide (CO), which are stronger ligands (SMLs, i.e. have higher binding constants) for a particular metal than the weaker metal ligand (WML) of the system.

System 9



System 10 depicts a similar type of assay, which results in a change in signal rather than a decrease in signal. For example, E_0 and λ could both change as a result of a new ligand binding.

System 10



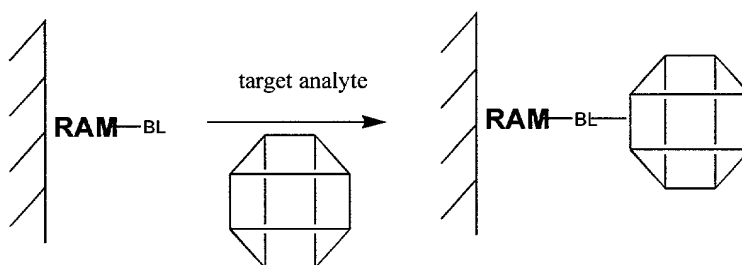
System 11 utilizes a change in the diffusion coefficient upon analyte binding for the change in faradaic impedance and mass transfer. In this embodiment, when the ligands are not covalently attached to an electrode, changes in the diffusion coefficient will alter the mass transfer impedance and thus the total faradaic impedance. That is, in some circumstances the frequency response of a redox active complex will be limited by its diffusion coefficient. Also, the charge transfer impedance may be altered by the binding of an analyte. At high frequencies, a redox active complex may not diffuse rapidly enough to reversibly transfer its electron to the electrode at a rate sufficient to generate a strong output signal. At low frequencies, the molecule has sufficient time to diffuse, and thus an output signal can be detected. In this embodiment, the use of monolayers is generally not preferred.

Thus, the result of binding to form an assay complex will generally alter the diffusion coefficient of the redox active molecule. As a result, the faradaic impedance will change. This effect will be greatest when the binding partner is large in comparison to the redox active moiety; the redox active moiety will go from being relatively small, and thus diffusing quickly, to relatively large upon binding into a

complex, and diffusing much more slowly; this results in the greatest changes and is thus preferred. Similarly, binding partners of roughly equal size can also result in a detectable signal.

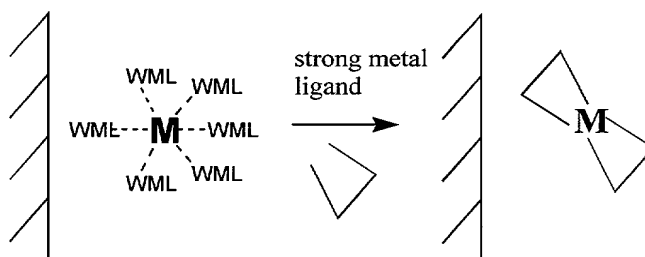
Alternatively, it is also possible that binding of the redox active moiety to its binding partner will cause a decrease in size. For example, some protein structures, i.e. antibodies, may have "loose" conformations that are sterically bulky, that "tighten up" as a result of binding to its partner (i.e. an antigen).

System 11



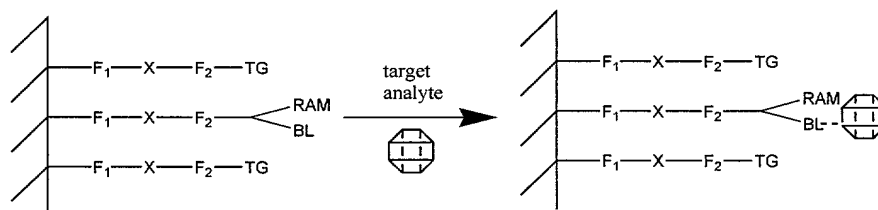
System 12 is similar to systems 10 and 11, as it is a sensor for different ligands, but it relies on a change in ligands to result in a change in E_0 of the system. A similar system may be used with two metals; that is, instead of adding strong metal ligands, a different metal, with different affinity for the ligands may be added, resulting in an electrochemical change.

System 12



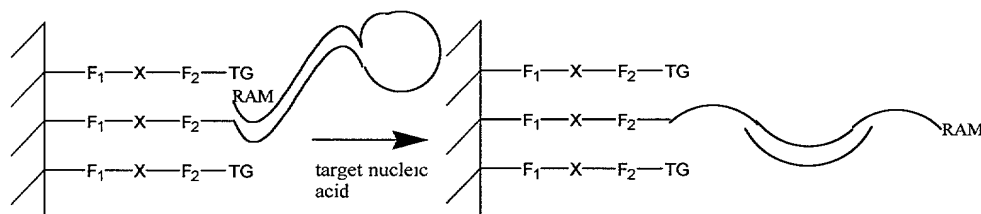
System 13 is a variation on previous systems, except that the RAM and the BL are closely associated or linked.

System 13



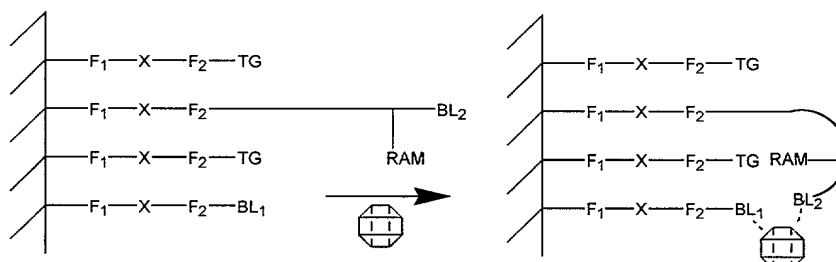
System 14 results in changes in faradaic impedance as a result of changes in E_0 or H_{AB} . In this case, the binding ligand will self-associate in some way, bringing the RAM into closer proximity to the electrode. For example, the binding ligand may be a nucleic acid (for example for the detection of a nucleic acid binding protein) or a protein (for example for the detection of proteins that inhibit or bind the binding ligand protein). Upon binding of the target, for example a protein, the conformation and thus the local environment of the RAM changes, resulting in a detectable signal. System 15 could also be run in "reverse", wherein the association of the analyte brings the RAM into proximity of the surface.

System 14



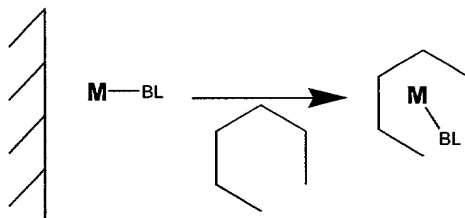
System 15 uses two binding ligands, BL_1 and BL_2 , which may be the same or different, to alter the environment of the RAM. It may be desirable to have one of the binding ligands be a somewhat "generic" binding ligand. Changes in E_0 and/or impedance will result in a detectable signal.

System 15



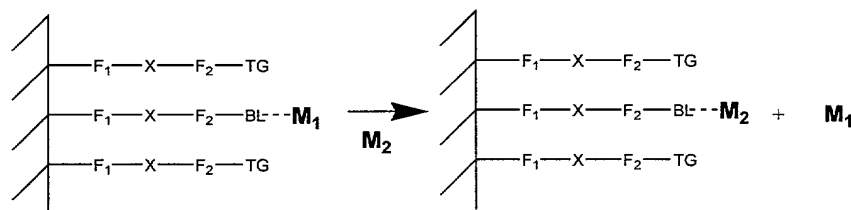
System 16 also relies on a decrease in signal. In this embodiment, a target analyte is used that will bind the metal ion-binding ligand complex in such a way as to render the metal unavailable to serve as a redox active molecule.

System 16



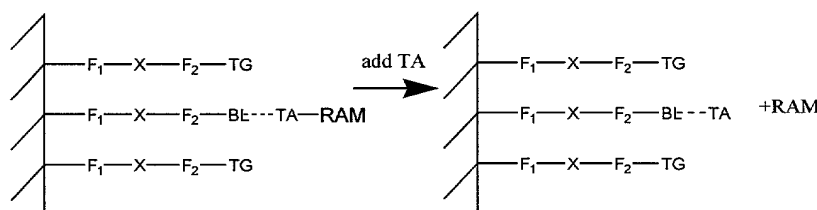
System 17 utilizes a change in metal ion affinity to a particular binding ligand to detect a change in the signal based on a different metal being present (resulting in a different E_0).

System 17



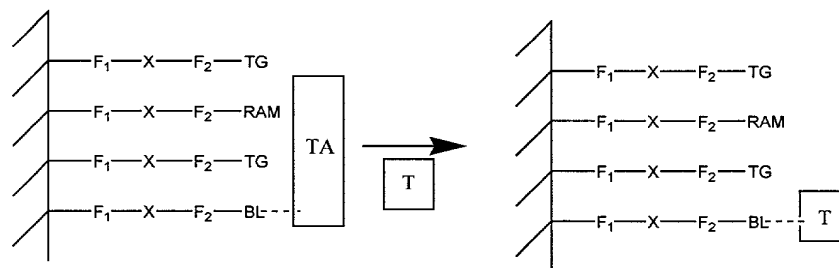
System 18 is similar to System 9 and depicts a competitive-type assay for detecting a target analyte. In System 15, a covalently attached target analyte or target analog (TA) is competed off of the binding ligand by the addition of the target analyte, resulting in a decrease in signal.

System 18



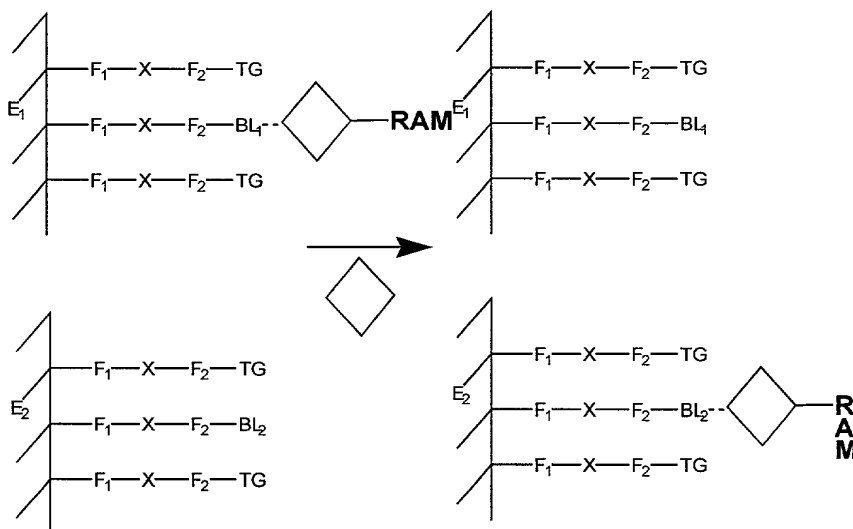
System 19 is a mixture of Systems 2 and 18, where the replacement of a bulky analog (TA) by a smaller target analyte (T) results in a different signal. For example, co-redoxant reactions could now occur. Alternatively, monolayers with "holes", that would allow current flow in the absence of the analog but do not in its presence, could also be used.

System 19



System 20 depicts a two electrode system in a competitive-type assay. This is useful in that it allows detection of an increase in signal on the second electrode, which is generally preferable to the loss of a signal.

System 20



As will be appreciated by those in the art, System 20 may also be configured in several different ways. BL1 and BL2 may have different affinities for the same site on the target analyte or analog, or bind to different sites. Similarly, the other systems may also be run in two electrode systems.

In addition, it is possible to use systems like those depicted above in several other embodiments. For example, since heat will change the faradaic impedance, the systems above could be used as a heat sensor. Similarly, attachment of the RAM to the electrode using a labile or cleavable bond can allow sensing of the cleaving agent based on a decrease in signal; for example, photolabile bonds can be used to detect light (uv); substrates can be used to sense enzymes (proteases, nucleases, carbohydrases, lipases, etc.) or other cleaving agents, such as drugs that cut nucleic acids, etc.

In the systems described above, the redox active complex is covalently attached to the electrode. This may be accomplished in any number of ways, as will be apparent to those in the art. In a preferred embodiment, one or both of the redox active molecule and the binding ligand are attached, via a spacer, to the electrode, using the techniques and compositions outlined below. By "spacer" herein is meant a moiety which holds the redox active complex off the surface of the electrode. In a preferred embodiment, the spacer used to attach the redox active molecule is a conductive oligomer as outlined herein, although suitable spacer moieties include passivation agents and insulators as outlined below. The spacer moieties may be substantially non-conductive. In general, the length of the spacer is as outlined for conductive polymers and passivation agents. As will be appreciated by those in the art, if the spacer becomes too long, the electronic coupling between the redox active molecule and the electrode will decrease rapidly.

In a preferred embodiment, the redox active molecule will be attached via a conductive oligomer, such that detection of changes in faradaic impedance as between the redox active molecule and the electrode can be detected. Other components of the system may be attached using other spacers; for example, when the binding ligand and the redox active molecule are attached separately, as is generally depicted in System 2, the binding ligand may be attached via a non-conductive oligomer spacer.

Once the assay complexes of the invention are made, that minimally comprise a target analyte and an ETM, and preferably a capture binding ligand, detection proceeds with electronic initiation. Without being limited by the mechanism or theory, detection is based on the transfer of electrons from the ETM to the electrode, including via the " π -way".

As outlined herein, the present invention is directed to the techniques that can be used to increase the signal, decrease the noise, or make the signal more obvious or detectable in a background of noise. That is, any technique that can serve to better identify a signal in the background noise may find use in the present invention. These techniques are generally classified in three ways: (1) variations in the type or methods of applying the initiation signals (i.e. varying the "input" to maximize or identify the sample signal); (2) data processing, i.e. techniques used on the "output" signals to maximize or identify the sample signal; and (3) variations in the assay itself, i.e. to the electrode surface or to the components of the system, that allow for better identification of the sample signal.

Detection of electron transfer, i.e. the presence of the ETMs, is generally initiated electronically, with voltage being preferred. A potential is applied to the assay complex. Precise control and variations in the applied potential can be via a potentiostat and either a three electrode system (one reference, one sample (or working) and one counter electrode) or a two electrode system (one sample and one

counter electrode). This allows matching of applied potential to peak potential of the system which depends in part on the choice of ETMs and in part on the conductive oligomer used, the composition and integrity of the monolayer, and what type of reference electrode is used. As described herein, ferrocene is a preferred ETM.

In a preferred embodiment, alternating current (AC) input signals are used. As described herein, a wide variety of different AC signals can be used. For example, the input signal can comprise only an AC component or both an AC component and a DC component, particularly a DC sweep. An AC voltage with a fundamental frequency f_0 is applied to the electrodes and the DC voltage is scanned through the redox potential of the ETM.

Without being bound by theory, it appears that ETMs, bound to an electrode, generally respond similarly to an AC voltage across a circuit containing resistors and capacitors. Basically, any methods which enable the determination of the nature of these complexes, which act as a resistor and capacitor, can be used as the basis of detection. Surprisingly, traditional electrochemical theory, such as exemplified in Laviron et al., J. Electroanal. Chem. 97:135 (1979) and Laviron et al., J. Electroanal. Chem. 105:35 (1979), both of which are incorporated by reference, do not accurately model the systems described herein, except for very small E_{AC} (less than 10 mV) and relatively large numbers of molecules. That is, the AC current (I) is not accurately described by Laviron's equation. This may be due in part to the fact that this theory assumes an unlimited source and sink of electrons, which is not true in the present systems.

The AC voltametry theory that models these systems well is outlined in O'Connor et al., J. Electroanal. Chem. 466(2):197-202 (1999), hereby expressly incorporated by reference. The equation that predicts these systems is shown below as Equation 1:

Equation 1

$$i_{avg} = 2nfFN_{total} \cdot \frac{\sinh\left[\frac{nF}{RT} \cdot E_{AC}\right]}{\cosh\left[\frac{nF}{RT} \cdot E_{AC}\right] + \cosh\left[\frac{nF}{RT} (E_{DC} - E_0)\right]}$$

In Equation 1, n is the number of electrons oxidized or reduced per redox molecule, f is the applied frequency, F is Faraday's constant, N_{total} is the total number of redox molecules, E_0 is the formal potential of the redox molecule, R is the gas constant, T is the temperature in degrees Kelvin, and E_{DC} is the electrode potential. The model fits the experimental data very well. In some cases the current is smaller than predicted, however this has been shown to be caused by ferrocene degradation which may be remedied in a number of ways.

In addition, the faradaic current can also be expressed as a function of time, as shown in Equation 2:

Equation 2

$$I_f(t) = \frac{q_e N_{total} n F}{2RT (\cosh [\frac{nF}{RT} (V(t) - E_0)] + 1)} \cdot \frac{dV(t)}{dt}$$

I_f is the Faradaic current and q_e is the elementary charge.

However, Equation 1 does not incorporate the effect of electron transfer rate nor of instrument factors. Electron transfer rate is important when the rate is close to or lower than the applied frequency. Thus, the true i_{AC} should be a function of all three, as depicted in Equation 3.

Equation 3

$$i_{AC} = f(\text{Nernst factors})f(k_{ET})f(\text{instrument factors})$$

These equations can be used to model and predict the expected AC currents in systems which use input signals comprising both AC and DC components. As outlined above, traditional theory surprisingly does not model these systems at all, except for very low voltages.

In general, non-specifically bound label probes/ETMs show differences in impedance (i.e. higher impedances) than when the label probes containing the ETMs are specifically bound in the correct orientation. In a preferred embodiment, the non-specifically bound material is washed away, resulting in an effective impedance of infinity. Thus, AC detection gives several advantages as is generally discussed below, including an increase in sensitivity, and the ability to "filter out" background noise. In particular, changes in impedance (including, for example, bulk impedance) as between non-specific binding of ETM-containing probes and target-specific assay complex formation may be monitored.

Accordingly, when using AC initiation and detection methods, the frequency response of the system changes as a result of the presence of the ETM. By "frequency response" herein is meant a modification of signals as a result of electron transfer between the electrode and the ETM. This modification is different depending on signal frequency. A frequency response includes AC currents at one or more frequencies, phase shifts, DC offset voltages, faradaic impedance, etc.

Once the assay complex including the target sequence and label probe is made, a first input electrical signal is then applied to the system, preferably via at least the sample electrode (containing the complexes of the invention) and the counter electrode, to initiate electron transfer between the electrode and the ETM. Three electrode systems may also be used, with the voltage applied to the reference and working electrodes. The first input signal comprises at least an AC component. The AC

component may be of variable amplitude and frequency. Generally, for use in the present methods, the AC amplitude ranges from about 1 mV to about 1.1 V, with from about 10 mV to about 800 mV being preferred, and from about 10 mV to about 500 mV being especially preferred. The AC frequency ranges from about 0.01 Hz to about 100 MHz, with from about 10 Hz to about 10 MHz being preferred, and from about 100 Hz to about 20 MHz being especially preferred.

The use of combinations of AC and DC signals gives a variety of advantages, including surprising sensitivity and signal maximization.

In a preferred embodiment, the first input signal comprises a DC component and an AC component. That is, a DC offset voltage between the working and counter electrodes is swept through the electrochemical potential of the ETM (for example, when ferrocene is used, the sweep is generally from 0 to 500 mV) (or alternatively, the working electrode is grounded and the counter electrode is swept from 0 to -500 mV). The sweep is used to identify the DC voltage at which the maximum response of the system is seen. This is generally at or about the electrochemical potential of the ETM. Once this voltage is determined, either a sweep or one or more uniform DC offset voltages may be used. DC offset voltages of from about -1 V to about +1.1 V are preferred, with from about -500 mV to about +800 mV being especially preferred, and from about -300 mV to about 500 mV being particularly preferred. In a preferred embodiment, the DC offset voltage is not zero. On top of the DC offset voltage, an AC signal component of variable amplitude and frequency is applied. If the ETM is present, and can respond to the AC perturbation, an AC current will be produced due to electron transfer between the electrode and the ETM.

For defined systems, it may be sufficient to apply a single input signal to differentiate between the presence and absence of the ETM (i.e. the presence of the target sequence) nucleic acid. Alternatively, a plurality of input signals are applied. As outlined herein, this may take a variety of forms, including using multiple frequencies, multiple DC offset voltages, or multiple AC amplitudes, or combinations of any or all of these.

Thus, in a preferred embodiment, multiple DC offset voltages are used, although as outlined above, DC voltage sweeps are preferred. This may be done at a single frequency, or at two or more frequencies.

In a preferred embodiment, the AC frequency is varied. At different frequencies, different molecules respond in different ways. As will be appreciated by those in the art, increasing the frequency generally increases the output current. However, when the frequency is greater than the rate at which electrons may travel between the electrode and the ETM, higher frequencies result in a loss or

decrease of output signal. At some point, the frequency will be greater than the rate of electron transfer between the ETM and the electrode, and then the output signal will also drop.

In a preferred embodiment, multiple frequencies with a small AC voltage is applied and the fundamental of each is evaluated. Alternatively, a preferred embodiment utilizes several frequencies with a large ACV, and the harmonics of each are evaluated. Similarly, preferred embodiments utilize several frequencies with a large ACV where the effect of the different frequencies on the system can result in an output that is different from the sum of the outputs at individual frequencies.

In one embodiment, detection utilizes a single measurement of output signal at a single frequency. That is, the frequency response of the system in the absence of target sequence, and thus the absence of label probe containing ETMs, can be previously determined to be very low at a particular high frequency. Using this information, any response at a particular frequency, will show the presence of the assay complex. That is, any response at a particular frequency is characteristic of the assay complex. Thus, it may only be necessary to use a single input frequency, and any changes in frequency response is an indication that the ETM is present, and thus that the target sequence is present.

In a preferred embodiment, the input signals and data processing steps are done to increase the non-linearity of the system. That is, for example, the ferrocene response reacts non-linearly, producing a harmonic response in the signal above that in the background; this harmonic signal from AC voltammetry is most likely the result of a harmonic distortion due to the nonlinear response of the electrochemical cell; see Yap, J. of Electroanalytical Chem. 454:33 (1998); hereby incorporated by reference. Thus, any techniques that increase this non-linearity are desirable. In a preferred embodiment, techniques are used to increase the higher harmonic signals; thus, frequency and phase-sensitive lock-in detection is performed at both the fundamental frequency of the applied waveform and also at multiples of the fundamental frequency (i.e. the higher harmonics). Since the background capacitance responds relatively linearly to AC signals (a sine wave input AC voltage results in a relatively nondistorted sine wave output), very little upper harmonic current is produced in the background. This gives a dramatic increase in the signal to noise ratio. Thus, detection at the higher harmonic frequencies, particularly the third, fourth and fifth harmonics (although the harmonics from second to tenth or greater can also be used) is shown to result in dramatic suppression of the background currents associated with non-Faradaic processes (like double layer charging) that can overwhelm the signal from the target molecules. In this way, the evaluation of the system at higher harmonic frequencies and phases can lead to significant improvements in the detection limits and clarity of signal. However, in some embodiments, the analysis of higher harmonics is not desired.

Thus, in a preferred embodiment, one method of increasing the non-linear harmonic response is to increase or vary the amplitude of the AC perturbation, although this may also be used in monitoring the fundamental frequency as well. Without being bound by theory, it appears that increasing the amplitude increases the driving force nonlinearly. Thus, generally, the same system gives an improved response (i.e. higher output signals) at any single frequency through the use of higher overpotentials at that frequency. Thus, the amplitude may be increased at high frequencies to increase the rate of electron transfer through the system, resulting in greater sensitivity. In addition, this may be used, for example, to induce responses in slower systems such as those that do not possess optimal spacing configurations.

In a preferred embodiment, measurements of the system are taken at at least two separate amplitudes or overpotentials, with measurements at a plurality of amplitudes being preferred. As noted above, changes in response as a result of changes in amplitude may form the basis of identification, calibration and quantification of the system. In addition, one or more AC frequencies can be used as well. Equation 4 describes the current output of a reversible surface redox reaction for any arbitrary driving potential V:

Equation 4

$$I_F(t) = \frac{q_e N_{tot} nF}{2RT \{ \cosh[\frac{nF}{RT}(V - E_0)] + 1 \}} \cdot \frac{dV}{dt}$$

This substitutes the Nernst distribution into (current) = (elementary charge)(change in number of oxidized molecules w.r.t. time); see O'Connor et al, J. Electroanal. Chem. 466:197 (1999), incorporated by reference. In AC voltammetry the driving voltage is an AC signal superimposed on a DC ramp, as depicted in Equation 5:

Equation 5

$$V(t) = V_i + rt + \epsilon_{AC} \sin(\omega t + \phi)$$

This leads to the following expression for I(t) (Equation 6):

Equation 6

$$I_F(t) = \frac{q_e N_{tot} nF}{2RT} \cdot \frac{r + \omega \epsilon_{AC} \cos(\omega t + \phi)}{\cosh\{\frac{nF}{RT}[V_i + rt - E_0 + \epsilon_{AC} \sin(\omega t + \phi)]\} + 1}$$

Calculated from the above expression, the Faradaic current around $E_0 = 200$ mV for a system of 10^6 surface redox molecules at 295 K being scanned with a 100 mV/s DC ramp and a 100 Hz 25 mV AC oscillation is shown in Figure 2A. This system's output is quite linear, with the Faradaic response being mostly sinusoidal (and 90- degree out of phase with the driving force). This is because there is only a 21% variation in the number of electrons available at $E_0 \pm 25$ mV (the FWHM of the Nernst

distribution is 90 mV at 295K with $n=1$). If instead an AC amplitude of 100 mV is used, the equation yields the scan shown in Figure 2B, with the data being shown in Figure 2C for the frequency spectrum and fourth harmonic AC voltammogram of a surface bound DNA system excited by $V_{ac} = 100$ mV. The non-linearity observed is caused by the fact that a large fraction of the Nernst distribution is being swept, with the number of redox electrons available at the extremes of the oscillation being only 7.5% of those available at E_0 . Since the response is not purely sinusoidal, it has harmonic components that are measured by locking into a higher frequency than the driving frequency. In addition, the symmetry of the signal changes as a function of DC potential. Figure 2D depicts the same signal as Figure 2C, but at a V_{DC} roughly 150 mV below E_0 . It is these variations in symmetry as a function of DC voltage that gives rise to the peak patterns and nodes that are observed when measuring harmonic scans in the present invention.

In a preferred embodiment, harmonic square wave ACV is used; see Baranski et al., J. Electroanal. Chem. 373:157 (1994), incorporated herein by reference, although in some embodiments this is not preferred. This gives several potential advantages. For example, square waves are easier to create digitally and the pulse shape of the square wave can allow for better discrimination against charging capacitance. In sinusoidal harmonic AC voltammetry, harmonic signals provide better signal to background since faradaic response can be more nonlinear than charging capacitance. The same concept applies to SW harmonic ACV. The key difference between the two techniques is the frequency spectrum of the AC waveform. A singular frequency sinusoidal waveform contains just the fundamental frequency where as a singular square wave contains the fundamental frequency as well as all odd harmonics. The technique looks at the even harmonics where the ratio of faradaic current to capacitance current is enhanced. All the odd harmonics have single ACV peaks while all the even harmonics have double ACV peaks. This is opposite to the case of sinusoidal harmonic ACV of a system that has a non-reversible redox couple. See Figure 3.

In a preferred embodiment, multiple frequency ACV is used. The idea is to create a waveform consisting of multiple frequencies with the same amplitude or different amplitudes to excite an electrochemical cell in an ACV fashion. The method benefits from fast Fourier transform or joint time-frequency transform to analyze the cell response. A JTFT spectrogram of a multiple frequencies ACV provides information on the driven (or fundamental) frequencies as well as their harmonic components. Some possible data analyses are: 1) comparison of response of fundamental frequencies, 2) comparison of all harmonic frequencies, 3) comparison of the response of one particular harmonic frequency of all excited frequencies, and 4) all analyses possible by standard single frequency ACV.

Accordingly, in a preferred embodiment, a fast Fourier transform is done, as is generally outlined in the examples. Fourier transform analysis is a preferred method for improving signal to noise and isolating desired signals when sinusoidal electrochemistry is done. Typical AC techniques rely on measurements of the primary frequency only. With sinusoidal voltammetry (and other inputs) observation at higher harmonics allows discrimination of signals primarily based on kinetics. For example, both fast and slow redox events would give similar peaks (provided the AC frequency was not too high) at the primary frequency. However, at higher harmonics, some redox molecules would generate signals while others would not. Using FFT analysis, all the various frequency components of a response to a sinusoidal input can be observed at once.

Similarly, in a preferred embodiment, a joint time-frequency transform (JTFT) is done, as is generally outlined in the Examples.

The use of multiple frequencies AC excitation waveform requires careful selection of the individual frequencies. Since the response of an electrochemical cell can be highly nonlinear, "unexcited" frequencies resulting from modulation of the base frequencies and their harmonics may produce erroneous Fourier transform data analysis if these unexcited frequencies coincide with any fundamental frequencies. Furthermore, with any waveform having multiple frequencies, the amplitude of the individual frequencies can differ greatly, depending on the phase relationship of the individual sinusoidal. The trick is to create a waveform with the smallest overall excitation amplitude while keeping the individual amplitudes as largest and as close to each other as possible. An example is to create a multiple frequency sinusoidal waveform with optimized phases (by minimizing constructive and destructive interference as well as modulation) and minimizes the total amplitude of the summed sine waves. Using technique similar to the Monte Carlo method one can use a random generator to perform phase optimization. For a waveform with n frequencies, $n-1$ harmonics is chosen that have the lowest probability of inter-modulation. A random generator is then used to generate $n-1$ random phases for each frequency. Three waveforms are calculated using these random phases, one at the generated phase θ , one with $\theta + \pi/2$, and one with $\theta + \pi/2$. An iteration routine is then used to identify and chose the waveform with the smallest absolute value of the amplitude from these waveforms. The procedure is repeated for $\pi/4$, $\pi/8$, ... $\pi/360$ or until we get to within one degree. It must be noted that this particular method can only locate a local minima but not necessarily the global minimum.

In a preferred embodiment, impedance analysis is done using data from a multiple frequencies ACV. This concept involves the use of an alternating current (AC) signal at various frequencies to excite the electrochemical cell; see Hazi et al., J. Electroanal. Chem. 437:1 (1997), hereby incorporated by reference. The multi-frequency AC signal is imposed on top of a DC staircase. Using fast Fourier transform, the cell's response is archived at each DC potential through the half-wave value.

Background subtraction is performed using impedance analysis of the cell response. The technique should allow for better discrimination against the charging current and the uncompensated solution resistance; see Baranski et al., J. Electrochemistry 453:29 (1998), hereby incorporated by reference.

In theory, the background current of the CMS electrochemical cell arises from charging electrical double layer with the charging current (I_c) being proportional to the rate of change of the applied potential dE/dt . as shown in Equation 7:

Equation 7

$$I^c = C_{dl} \frac{dE}{dt}$$

This "constant" proportionality factor is the familiar double-layer capacitance. The faradaic current, however, is proportional to the concentration c and the square root of the rate of change of the applied potential (see Laviron et al., J. Electroanal. Chem. 101:19 (1979), incorporated by reference) as depicted in Equation 8:

Equation 8:

$$I \propto \frac{dc}{dt} = c \sqrt{\frac{de}{dt}}$$

These two simple relationships show that as c decreases or the frequency of the AC excitation is raised, the background current may exceed the faradaic signal.

In the ideal limit, the charging and faradaic currents have different phase relations with respect to the applied excitation potential ($-\pi/2$ and $-\pi/4$, respectively). Hence, by plotting only the in-phase component (real part) of FFT of the cell output, the charging current can be rejected whereas the faradaic signal is only slightly reduced (this is essentially what a lock-in amplifier does). However, the efficiency of the discrimination against the charging current is strongly affected by the value of the "uncompensated" solution resistance R_u . The uncompensated solution resistance can alter the phase relations of both the charging and faradaic currents in a frequency dependent manner. Schiewe et al. (J. Electroanal. Chem. 451:129 (1998), hereby incorporated by reference) have shown that as the excitation frequency increases, the charging current increasingly contributes to the real part of the cell output. A similar phenomenon is seen in the present systems, where, as the ACV frequency is increased, the background impedance increases accordingly and the phase information is drastically altered (that is why it is preferable to use phase to discriminate the charging current when the excitation frequency and cycle is relatively low). Conceptually, it is difficult to evaluate and correct for

R_u with only single-frequency information. One can only extract R_u via impedance analysis and with the use of the Randles curves (real and imaginary part of the impedance versus $\omega^{-1/2}$).

There are generally two ways to correct for the charging current and the uncompensated resistance. Both the double layer capacitance and uncompensated resistance can be estimated from a negative control experiment where little or no faradaic reaction occurs. In this case, R_u is the real part of the cell impedance (Z') and C_{dl} is the slope of the plot $1/Z''$ versus ω , where Z'' is the imaginary part of the cell impedance. This scenario is probably not applicable to the present systems since the cell behavior changes from electrode to electrode. A more attractive approach involves "background" subtraction using a potential region where no faradaic process occurs within a scan; i.e. C_{dl} and R_u can be obtained from measurements taken at potentials that are more negative and more positive than the peak potential of the electron distribution-of-states Gaussian. Theoretically, R_u can be estimated, at any potential, from the extrapolated high frequency intercept of the measured impedance of the real component and C_{dl} can be estimated in the presence of a faradaic process from the magnitude of the admittance of high frequencies.

The presence of the ETMs at the surface of the monolayer can be detected in a variety of ways. A variety of detection methods may be used, including, but not limited to, optical detection (as a result of spectral changes upon changes in redox states), which includes fluorescence, phosphorescence, luminiscence, chemiluminescence, electrochemiluminescence, and refractive index; and electronic detection, including, but not limited to, amperometry, voltammetry, capacitance and impedance. These methods include time or frequency dependent methods based on AC or DC currents, pulsed methods, lock-in techniques, filtering (high pass, low pass, band pass), and time-resolved techniques including time-resolved fluorescence.

In one embodiment, the efficient transfer of electrons from the ETM to the electrode results in changes in the redox state of the ETM. With many ETMs including the complexes of ruthenium containing bipyridine, pyridine and imidazole rings, these changes in redox state are associated with changes in spectral properties. Significant differences in absorbance are observed between reduced and oxidized states for these molecules. See for example Fabbri et al., Chem. Soc. Rev. 1995 pp197-202). These differences can be monitored using a spectrophotometer or simple photomultiplier tube device.

In this embodiment, possible electron donors and acceptors include all the derivatives listed above for photoactivation or initiation. Preferred electron donors and acceptors have characteristically large spectral changes upon oxidation and reduction resulting in highly sensitive monitoring of electron transfer. Such examples include $Ru(NH_3)_4py$ and $Ru(bpy)_2im$ as preferred examples. It should be

understood that only the donor or acceptor that is being monitored by absorbance need have ideal spectral characteristics.

In a preferred embodiment, the electron transfer is detected fluorometrically. Numerous transition metal complexes, including those of ruthenium, have distinct fluorescence properties. Therefore, the change in redox state of the electron donors and electron acceptors attached to the nucleic acid can be monitored very sensitively using fluorescence, for example with $\text{Ru}(4,7\text{-biphenyl}_2\text{-phenanthroline})_3^{2+}$. The production of this compound can be easily measured using standard fluorescence assay techniques. For example, laser induced fluorescence can be recorded in a standard single cell fluorimeter, a flow through "on-line" fluorimeter (such as those attached to a chromatography system) or a multi-sample "plate-reader" similar to those marketed for 96-well immuno assays.

Alternatively, fluorescence can be measured using fiber optic sensors with nucleic acid probes in solution or attached to the fiber optic. Fluorescence is monitored using a photomultiplier tube or other light detection instrument attached to the fiber optic. The advantage of this system is the extremely small volumes of sample that can be assayed.

In addition, scanning fluorescence detectors such as the FluorImager sold by Molecular Dynamics are ideally suited to monitoring the fluorescence of modified nucleic acid molecules arrayed on solid surfaces. The advantage of this system is the large number of electron transfer probes that can be scanned at once using chips covered with thousands of distinct nucleic acid probes.

Many transition metal complexes display fluorescence with large Stokes shifts. Suitable examples include bis- and trisphenanthroline complexes and bis- and trisbipyridyl complexes of transition metals such as ruthenium (see Juris, A., Balzani, V., et. al. *Coord. Chem. Rev.*, V. 84, p. 85-277, 1988). Preferred examples display efficient fluorescence (reasonably high quantum yields) as well as low reorganization energies. These include $\text{Ru}(4,7\text{-biphenyl}_2\text{-phenanthroline})_3^{2+}$, $\text{Ru}(4,4'\text{-diphenyl-2,2'-bipyridine})_3^{2+}$ and platinum complexes (see Cummings et al., *J. Am. Chem. Soc.* 118:1949-1960 (1996), incorporated by reference). Alternatively, a *reduction* in fluorescence associated with hybridization can be measured using these systems.

In a further embodiment, electrochemiluminescence is used as the basis of the electron transfer detection. With some ETMs such as $\text{Ru}^{2+}(\text{bpy})_3$, direct luminescence accompanies excited state decay. Changes in this property are associated with nucleic acid hybridization and can be monitored with a simple photomultiplier tube arrangement (see Blackburn, G. F. *Clin. Chem.* 37: 1534-1539 (1991); and Juris et al., *supra*).

In a preferred embodiment, electronic detection is used, including amperometry, voltammetry, capacitance, and impedance. Suitable techniques include, but are not limited to, electrogravimetry; coulometry (including controlled potential coulometry and constant current coulometry); voltammetry (cyclic voltammetry, pulse voltammetry (normal pulse voltammetry, square wave voltammetry, differential pulse voltammetry, Osteryoung square wave voltammetry, and coulostatic pulse techniques); stripping analysis (anodic stripping analysis, cathodic stripping analysis, square wave stripping voltammetry); conductance measurements (electrolytic conductance, direct analysis); time-dependent electrochemical analyses (chronoamperometry, chronopotentiometry, cyclic chronopotentiometry and amperometry, AC polarography, chronogalvanometry, and chronocoulometry); AC impedance measurement; capacitance measurement; AC voltammetry; and photoelectrochemistry.

In a preferred embodiment, monitoring electron transfer is via amperometric detection. This method of detection involves applying a potential (as compared to a separate reference electrode) between the nucleic acid-conjugated electrode and a reference (or counter) electrode in the sample containing target genes of interest. Electron transfer of differing efficiencies is induced in samples in the presence or absence of target nucleic acid; that is, the presence or absence of the target nucleic acid, and thus the label probe, can result in different currents.

The device for measuring electron transfer amperometrically involves sensitive current detection and includes a means of controlling the voltage potential, usually a potentiostat. This voltage is optimized with reference to the potential of the electron donating complex on the label probe. Possible electron donating complexes include those previously mentioned with complexes of iron, osmium, platinum, cobalt, rhenium and ruthenium being preferred and complexes of iron being most preferred.

In a preferred embodiment, alternative electron detection modes are utilized. For example, potentiometric (or voltammetric) measurements involve non-faradaic (no net current flow) processes and are utilized traditionally in pH and other ion detectors. Similar sensors are used to monitor electron transfer between the ETM and the electrode. In addition, other properties of insulators (such as resistance) and of conductors (such as conductivity, impedance and capacitance) could be used to monitor electron transfer between ETM and the electrode. Finally, any system that generates a current (such as electron transfer) also generates a small magnetic field, which may be monitored in some embodiments.

It should be understood that one benefit of the fast rates of electron transfer observed in the compositions of the invention is that time resolution can greatly enhance the signal-to-noise results of monitors based on absorbance, fluorescence and electronic current. The fast rates of electron transfer of the present invention result both in high signals and stereotyped delays between electron

transfer initiation and completion. By amplifying signals of particular delays, such as through the use of pulsed initiation of electron transfer and "lock-in" amplifiers of detection, and Fourier transforms.

In a preferred embodiment, background subtraction of the current vector and phase optimization is done. The output from the electrochemical cell is essentially a current. It follows that any background subtraction of the current amplitude alone will be somewhat inaccurate and thus, it is better to subtract the capacitance current vector from the total current, not just the amplitude. Since the background subtraction scheme involves vectors, it is useful to scan the phase of these vectors to enhance signal to background. An example algorithm is as follows. A polynomial curve is simultaneously fitted to the background capacitance current vector and a search is performed in a binary fashion to find a phase at which the faradaic current vector is maximized. To sample the entire phase space, one only need to scan up to π and analyze the data every $8\pi/45$ at $0, 8\pi/45, 16\pi/45, 24\pi/45, 32\pi/45,$ and $8\pi/9$. The phase at which the signal is the largest is the new initial point for the next iteration. The algorithm then compares the last best phase θ_{last} with two new phases at $\theta_{last} \pm 4\pi/45$. The sequence is repeated for $\theta_{last} \pm 2\pi/45, \theta_{last} \pm \pi/45, \theta_{last} \pm \pi/90,$ and $\theta_{last} \pm \pi/180$. This method should allow for better peak detection when signal to background is small. Furthermore, the method is more effective at harmonics greater than fundamental since phase changes are greater at higher harmonics.

In a preferred embodiment, correlation and/or convolution techniques are used. In this embodiment, many scans of the same electrode. Rather than looking for a peak in a single scan, many scans are viewed and a common correlation between the scans. For instance, it is possible that a bump in the noise appears near 180 mV for a negative, even if no ferrocene is present. However, it is unlikely that the same bump will appear in the same place if the frequencies are scanned. Thus, preferred embodiments take scans at many frequencies and only count a positive if a peak occurs in all of them. This is a very simple correlation; more complex correlations may be done as well.

For example, a preferred embodiment utilizes a voltage $V(t)$ and apply it to a cell (electrode). The output signal $i(t)$ gets filtered to result in the data: $V(t) \times \text{Cell} = i(t) \times \text{filter} = \text{data}(t)$. A lock in amplifier may be used to do a simple notch filter; similarly, mathematical filters may be used such as FFT.

However, more complex analyses can be done. As outlined in the following table, a variety of filters may be used:

$$V(t) \times \text{Cell} = i(t) \times \text{filter}_1 = \text{data}_1(t)$$

$$V(t) \times \text{Cell} = i(t) \times \text{filter}_2 = \text{data}_2(t)$$

$$V(t) \times \text{Cell} = i(t) \times \text{filter}_3 = \text{data}_3(t)$$

$$V(t) \times \text{Cell} = i(t) \times \text{filter}_4 = \text{data}_4(t)$$

$$V(t) \times \text{Cell} = i(t) \times \text{filter}_5 = \text{data}_5(t)$$

$$V(t) \times \text{Cell} = i(t) \times \text{filter}_6 = \text{data}_6(t)$$

$$V(t) \times \text{Cell} = i(t) \times \text{filter}_7 = \text{data}_7(t)$$

All of the data sets may be subjected to another mathematical filter:

$$\text{data}_1 \otimes \text{data}_2 \otimes \text{data}_3 \otimes \text{data}_4 \otimes \text{data}_5 \otimes \text{data}_6 \otimes \text{data}_7 = \text{data}_{\text{final}}$$

The individual data files may not even look like peaks. But, when correlated together, the $\text{data}_{\text{final}}$ can have a characteristic response that is unique to target analyte signals. The simplest example is to have all of the filters the same and the final correlation is simply an average. Alternatively, the waveforms applied can be altered:

$$V_1(t) \times \text{Cell} = i(t) \times \text{filter}_1 = \text{data}_1(t)$$

$$V_2(t) \times \text{Cell} = i(t) \times \text{filter}_2 = \text{data}_2(t)$$

$$V_3(t) \times \text{Cell} = i(t) \times \text{filter}_3 = \text{data}_3(t)$$

$$V_4(t) \times \text{Cell} = i(t) \times \text{filter}_4 = \text{data}_4(t)$$

$$V_5(t) \times \text{Cell} = i(t) \times \text{filter}_5 = \text{data}_5(t)$$

$$V_6(t) \times \text{Cell} = i(t) \times \text{filter}_6 = \text{data}_6(t)$$

$$V_7(t) \times \text{Cell} = i(t) \times \text{filter}_7 = \text{data}_7(t)$$

Again, a correlation on the data can be run to get $\text{data}_{\text{final}}$.

An example here is the frequency response curve; the application of 100 Hz with a 100 Hz filter, 1 kHz with a 1 kHz filter, etc. then the peak information is plotted. A characteristic curve of the peak information means a positive.

As outlined herein, the electrode signal of each cell is actually broken up into $\text{cell} = i_{\text{ferrocene}} + i_{\text{capacitance}} + i_{\text{noise}}$. This may be used since the $i_{\text{ferrocene}}$ should be the only part that has a Nernstian distribution always centered around $E_{1/2}$. Mathematically, preferred embodiments determine the optimal value of $V_1(t)$ etc and filter₁, etc. and perform mathematical correlations on the data. Ferrocene is used only by way of example of a preferred ETM.

In a preferred embodiment, signal recovery is done using signal recognition and background subtraction. In this embodiment, the idea is to fit the cell response to two functions, one that describes the signal and the other that models the background. Once the functions are constructed, the signal is easily recovered from the response by subtracting the background. This signal recognition scheme is applicable to any system where the signal has a behavior that is relatively well known. The following example illustrates how such a scheme can be applied to the systems of the invention.

The response from an electrochemical cell can be processed with a lock-in amplifier. This is one of many methods of increasing signal to background using some form of bandwidth-narrowing technique. The fourth harmonic component of the cell response can be represented by two current vectors $X(v_{dc})$ and $Y(v_{dc})$. The 4th harmonic $X(v_{dc})$ and $Y(v_{dc})$ components of the current are approximated by two curves, each composed of the sum of two functions (Equations 9 and 10):

$$F_x(v) = F_{1x}(v) + F_{2x}(v) = G'''(A_{x0}, A_{x1}, A_{x2}, v) + A_{x3} + A_{x4}v + A_{x5}v^2 + A_{x6}v^3 + A_{x7}v^4 + A_{x8}v^5$$

$$F_y(v) = F_{1y}(v) + F_{2y}(v) = G'''(A_{y0}, A_{y1}, A_{y2}, v) + A_{y3} + A_{y4}v + A_{y5}v^2 + A_{y6}v^3 + A_{y7}v^4 + A_{y8}v^5$$

The first part of the curve ($F_{1i}(v_{dc})$) is the third derivative of a modified Gaussian distribution which approximates the fourth harmonic of the faradaic signal. The second component, ($F_{2i}(V)$) is a 5th order polynomial which approximates the background.

The analytical expression for the modified Gaussian distribution used in the algorithm is shown in Equation 11:

Equation 11

$$G(A_0, A_1, A_2, v) = A_0 E^{-(v-A_2)^2 A_1^2}$$

Accordingly, the third derivative of Equation 11 is given by Equation 12:

Equation 12

$$G'''(A_0, A_1, A_2, v) = 4A_0 A_1^4 E^{-(v-A_2)^2 A_1^2} (3 - 2A_1^2 (A_2 - v)^2)(v - A_2)$$

The third derivative of the modified Gaussian (12) depends on three parameters: A_0 controls the amplitude of the signal; A_1 determines the width of the curve as well as the amplitude; and A_2 is the center, or mean, of the signal. The maximum amplitude of the central peaks of the third derivative of the modified Gaussian is a function of the A_0 and A_1 according to the relation (Equation 13):

Equation 13

$$G'''_{\max} = 4\sqrt{9 - 3\sqrt{6}} A_0 A_1^3 E^{\sqrt{\frac{3}{2}} \frac{3}{2}} \approx 3.9 A_0 A_1^3$$

This value in Eq. 13 is obtained by evaluating the third derivative of the modified Gaussian at the zeroes of the fourth derivative of the modified Gaussian. The zeroes of the fourth derivative of the modified Gaussian are given by the expression (Equation 14):

Equation 14

$$v_{1,2,3,4} = A_2 \pm \frac{\sqrt{2}\sqrt{3 \pm \sqrt{6}}}{2A_1}$$

Equation 14 illustrates how A_0 and A_1 determine the amplitude of the signal in fourth harmonic.

Curve fitting and peak recognition can be achieved by modeling the data (see Press et al., Numerical Recipes in C, The Art of Scientific Computing, 2d Ed., N.Y. Cambridge University Press (1996); Forsyth et al, Computer Methods for Mathematical Computations (1977)) using linear models such as the Least squares method (Lawson et al., Solving Least Squares Problems, N.J. Prentice Hall (1974)) and Chi-square fitting (Bevington et al., Data Reduction and Error Analysis for the Physical Sciences, N.Y. McGraw Hill (1969); von Mises Mathematical Theory of Probability and Statistics, NY Academic Press (1964)) or nonlinear models such as Levenberg-Marquardt (Marquardt, J. of the Society for Industrial and Applied Mathematics vol. 11, pp431-441) and other nonlinear least-squares (More, Numerical Analysis, Lecture Notes in Mathematics, vol. 630 Watson, Berlin: Springer-Verlag) methods. In our example we use the Levenberg-Marquardt algorithm to find the optimal set of A_x 's and A_y 's that best fit Eq. 9 to the current vectors $X(v_{dc})$ and $Y(v_{dc})$. We define two error coefficients for $X(v_{dc})$ and $Y(v_{dc})$ and equations 9 and 10 as Equations 15 and 16:

$$E_x = \sum_i \frac{(X_{\text{true}}(v_i) - X_{\text{fit}}(A_{x0}, A_{x1}, A_{x2}, A_{x3}, A_{x4}, A_{x5}, A_{x6}, A_{x7}, A_{x8}, v_i))^2}{\sigma_{xi}^2}$$

$$E_y = \sum_i \frac{(Y_{\text{true}}(v_i) - Y_{\text{fit}}(A_{y0}, A_{y1}, A_{y2}, A_{y3}, A_{y4}, A_{y5}, A_{y6}, A_{y7}, A_{y8}, v_i))^2}{\sigma_{yi}^2}$$

The standard deviations σ provides the weighting of points of the data set, and are usually set to 1. The optimum set of parameters (A 's) will be such that the error coefficients are minimized. That happens when the derivatives of the error coefficients equal zero.

Equations 17 and 18

$$\nabla E_x = \frac{\partial E_x}{\partial A_{xn}} = -2 \sum_i \frac{\frac{\partial X_{\text{fit}}(A_x, v_i)}{\partial A_{xn}} (X_{\text{data}}(v_i) - X_{\text{fit}}(A_x, v_i))}{\sigma_{xi}^2} = 0$$

$$\nabla E_y = \frac{\partial E_y}{\partial A_{yn}} = -2 \sum_i \frac{\frac{\partial Y_{\text{fit}}(A_y, v_i)}{\partial A_{yn}} (Y_{\text{data}}(v_i) - Y_{\text{fit}}(A_y, v_i))}{\sigma_{yi}^2} = 0$$

The second derivatives of the error coefficients after dropping second terms are Equations 19 and 20:

$$\nabla \nabla E_x = \frac{\partial^2 E_x}{\partial A_{xn}^2} \approx 2 \sum_i \frac{\frac{\partial X_{\text{fit}}(A_x, v_i)}{\partial A_{xn}} \frac{\partial X_{\text{fit}}(A_x, v_i)}{\partial A_{xn}}}{\sigma_{xi}^2} = 0$$

$$\nabla \nabla E_y = \frac{\partial^2 E_y}{\partial A_{yn}^2} \approx 2 \sum_i \frac{\frac{\partial Y_{fit}(A_y, v_i)}{\partial A_{yn}} \frac{\partial Y_{fit}(A_y, v_i)}{\partial A_{yn}}}{\sigma_{yi}^2} = 0$$

Expanding equations 19 and 20 in a Taylor series we obtain the following matrices:

Equation 21 and 22:

$$\nabla E_x(A_x) = \nabla E_x(A_{x-initial}) + \nabla \nabla E_x(A_{x-initial})(A_{x-initial} - A_x) = 0$$

$$\nabla E_y(A_y) = \nabla E_y(A_{y-initial}) + \nabla \nabla E_y(A_{y-initial})(A_{y-initial} - A_y) = 0$$

That can be expressed as Equation 23:

$$\sum_{l=0}^8 \alpha_{kl} \delta A_l = \beta_k$$

The Levenberg - Marquardt method incorporates a dimensionless parameter λ to the diagonal of matrix α to speed up convergence. The new matrix is then defined by Equation 24

$$\begin{aligned} \alpha'_{jj} &\equiv \alpha_{jj}(1 + \lambda) \\ \alpha'_{kj} &\equiv \alpha_{kj} \quad \text{for } k \neq j \end{aligned}$$

The system of equation is solved by a Newton-Raphson (Acton, Numerical methods that work, Washington: Mathematical Association of America, 1990; Press, supra) iterative scheme. With a good initial guess of A's the method converges to the optimal set of A's that best represent the data.

An example of a signal recognition algorithm is as follows. After the data is read in, the application first attempts to find a "good fit" for X. A "good fit" is determined by a number of parameters including, but not limited to, a minimal mean square error (MSE) between the "true" scan and the "best fit" (see Discrimination Procedure below). At present the application first attempts to fit X at 0 degrees. If this fit is a "bad" fit (e.g., high MSE), the application then attempts to fit X at 45 degrees. If this too is a "bad" fit, the application is unable to find a signal (peak) in X and, at present, is unable to solve for I_p or E_o . Under these conditions, the application generates an error code (-999) and performs no further analysis.

If a "good fit" is found for X, the application then attempts to find a "good fit" for Y. If, and only if, the application is able to find a "good fit" for X and Y at the same angle, will it continue to solve for I_p and E_o . At present, if the application is unable to find a "good fit" for X and Y at the same angle, it generates an error code (-999) and performs no further analysis. It is also possible to fit to just one current vector but this particular algorithm presently requires two vectors for analysis. Removing the two vectors constraint should allow for recognition when signal to background ratio is very small.

To determine a “good fit” for either X or Y, the application must first define an initial “guess” for the 9 coefficients used by the fitting algorithm. This initial guess must be made for both X and Y at each angle. Furthermore, this initial “guess” must be based upon the original data and the previously described characteristics of the 3rd derivative of the Gaussian.

Initial guesses are as follows. An initial 5th order polynomial is fit to the data using the Singular Value Decomposition method (Press, supra). This polynomial is subtracted from the “original” data (X or Y). If we assume that the maximum and minimum of this curve correspond to the central peaks of the Gaussian, and that the positions of the central peaks are given by v_2 and v_3 in Eq. 14, we can then obtain a good initial guess for the fitting of the third derivative of the modified Gaussian by Equation 24:

Equation 24

$$\begin{aligned} A_2 &= \frac{v_2 + v_3}{2} \\ A_1 &= \frac{\sqrt{2(3 - \sqrt{6})}}{|v_3 - v_2|} \\ A_0 &= \frac{|X_{\text{data}}(v_3) - X_{\text{data}}(v_2)|}{7.8A_1^3} \end{aligned}$$

Often, the satellite peaks of the signal are mistaken as the central peak and hence the algorithm fails to fit the data. This “failure” is detected by checking Equation 25:

Equation 25:

$$\left| \frac{(X_{\text{true}}(v_{p2}) - X_{\text{fit}}(v_{p2}) + X_{\text{true}}(v_{p3}) - X_{\text{fit}}(v_{p3}))}{7.8A_0A_1^3} \right| > K = 1/4$$

If Equation 25 is true, this indicates that the satellite peaks of the fit are separated from the true data by more than 1/4 of the amplitude of the Gaussian fit. Under these conditions, we defined two parameters (Equations 26 and 27):

Equations 26 and 27

$$\xi = \text{sign}[A_0 \{X_{\text{true}}(v_{p2}) - X_{\text{fit}}(v_{p2}) + X_{\text{true}}(v_{p3}) - X_{\text{fit}}(v_{p3})\}]$$

$$D = \frac{\sqrt{2(3 - \sqrt{6})}}{A_1}$$

where D is was obtained from Eq. 14, and is the distance between the two central peaks of the third derivative of the modified Gaussian. We then attempted a new fit with the same initial conditions but with Equations 28 and 29:

Equations 28 and 29

$$A_0^{new} = -A_0^{old}$$

$$A_2^{new} = A_2^{old} + D^{\xi}$$

If this second fit failed or Equation 25 was not true, then a third set of initial conditions was launched to fit the data. The third set of initial conditions was the same as the first with one exception: $A_0 = -1$.

A number of criteria are used to determine if a set of calculated coefficients provides a "good fit" for either X or Y. These criteria, which are applied in a specific order for both X and Y, are as follows (in the order of application). Criteria 1 requires that for a good fit, the difference between the "true" data and the fit must be minimal. Hence, we compute a weighted mean square error term, where the MSE is weighted by the amplitude of the Gaussian component of the data in Equations 30 and 31 (this value is obtained by taking the different between the maximum and the minimum of the data minus the preliminary 5th order polynomial fit):

Equations 30 and 31

$$MSE_{weighted} = \frac{\frac{MSE}{(Max(X_{true} - X_{5^{th} poly}) - min(X_{true} - X_{5^{th} poly}))^2}}{\frac{\sum_{i=1}^n (Y_{true} - Y_{fit})^2}{n(Max(X_{true} - X_{5^{th} poly}) - min(X_{true} - X_{5^{th} poly}))^2}} =$$

This weighted MSE error should be less than 1×10^{-3} . If it is not, we redefine, as described above, some of the coefficients and re-fit the data.

The second criteria is that for a "good fit," the width of the Gaussian term (A_1) is typically between 12 and 14. The algorithm requires $10 < A_1 < 20$ for any fit to be classified as a good fit.

If the fit has past the first two criteria, than the weighted MSE must be less than 1×10^{-2} . If either condition 2 or 3 fail, the application changes the angle (from 0 to 45 degrees) and attempts, once again, to satisfy all 3 criteria (1-3). As mentioned above, if the application is unable to satisfy all 3 criteria at 0 and 45 degrees for either X or Y, it is unable to solve for I_p and E_o (error code = -999)

If a “good fit” has been found for both X and Y (i.e., the fit for X and Y has passed criteria 1 through 3), then the application applies two final criteria: one to compare the fit for X to the fit for Y and one to compare the fit for R to the “true” R (scan). To compare the fit for X to the fit for Y, the application examines the difference between the calculated (A_{2x} and A_{2y}) E_o locations for X and Y. The absolute difference between these two values must be no greater than 50 milli-volts. This value ensures that the fitting algorithm is not fitting the central peak to the satellite peaks of the data in either X or Y. The distance between peaks is given by the position of the extreme of the third derivative of the modified Gaussian.

It is possible to (“locked-in”) to a “wrong” peak in either X or Y. For example, if X had a peak at 180 mV and one at 250 mV, the application may fit (find) the peak at 225 mV, causing the absolute difference in the E_o s to be greater than 50 mV if the E_o for Y was found at 180 mV. To account for this case, if the absolute difference between the E_o s is greater than 50 mV, the code shifts (via A_2), invert ($A_o = -A_o$) and re-fit the signal (X or Y) that is farthest from a user-defined expected E_o . The shift is in the direction of the expected E_o . If shifting and inverting improves (<weighted MSE) the fit, we use the newly found coefficients; otherwise, the code returns to the previous coefficients and report an E_o separation error (Error Code = -777).

To compare the fit for R to the true R (scan), we compute the I_p divided by the RMS of the fit in Equation 32:

Equation 32

$$\frac{I_p}{\sqrt{\sum_i \frac{(R_{data} - R_{fit})^2}{n}}} > K = 3.7$$

The value in Eq. 32 was determined empirically. If the I_p /RMS is less than 3.70, the application provides an error code of -888.

In a preferred embodiment, the application is solved for I_p and E_o . In this version of the application, both X and Y must be fit in order to solve for I_p and E_o (a positive result). The reason is that the amplitude in R is defined as Equation 33:

Equation 33

$$R(v) = \sqrt{X^2(v) + Y^2(v)}$$

It is possible to extract the R amplitude from only one component (either X or Y alone) using the relation of Equation 34:

Equation 34

$$R(v) = \frac{X(v)}{\cos(\theta)}$$

However, if the phase information is poor, Eq. 34 is difficult to reconstruct. Once fits for X and Y are obtained, the peak height (I_p or G'''_{\max}) and center of the signal (E_0 or A_2) are given by the following equations 35 and 36:

Equations 35 and 36

$$G'''_{\max} = 4\sqrt{9 - 3\sqrt{6}} A_0 A_1^3 E^{1/2 - \frac{3}{2}} \approx 3.9 A_0 A_1^3$$

$$E^0_R = \frac{E^0_x I_x^2 + E^0_y I_y^2}{I_x^2 + I_y^2}$$

If the application is able to calculate I_p and E_0 with no errors, a positive indicator will be displayed (green light). If, on the other hand, the application is unable to calculate these values within the user-defined "settings" (Green/Yellow or Yellow/Red via the Constants control), then the indicator will be yellow (marginal positive) or red (a negative result).

In a preferred embodiment, spectral analysis of the signal is done. In this embodiment, filtering techniques in the frequency domain make use of means, variances, densities, autocorrelation functions, and power spectral densities of the signal and apply it to the present systems to enhance the signal to noise ration (see Schwartz et al., Signal Processing: Discrete Spectral Analysis, Detection, and Estimation, N.Y. McGraw Hill, 1975, hereby incorporated by reference).

In a preferred embodiment, digital filtering techniques are used. These include, but are not limited to, match filter, Weiner filtering, Kalman, Finite Impulse Response, infinite impulse response, narrow band filtering, etc.

In a preferred embodiment, a match filter is used; match filters are a signal processing technique that "weights" the measured response (signal plus noise) samples by some corresponding known signal amplitudes and adds them together to enhance signal to noise.

In a preferred embodiment, a weiner filter is used (see Press, supra; and Elliot et al., Fast Transforms: Algorithm, Analysis, Applications N.Y. Academic Press (1982), both of which are incorporated by reference). Weiner filtering involves finding an optimal filter that removes noise or background from the "corrupted" signal. This signal processing method works in conjunction with Fourier transform techniques. The idea is as follows. Due to poor signal to noise or a large background, the output from the instrument is a "corrupted" signal

$$c(t) = s(t) + n(t)$$

where $s(t)$ is the signal and $n(t)$ is the noise. Note that $s(t)$ is not the signal we're after, it is composed of the true uncorrupted signal $u(t)$ convolved with some known response function $r(t)$ (In the case of the CMS system with a redox couple, $r(t)$ is the Nernstian). In other words,

$$s(t) = \int_{-\infty}^{\infty} r(t-\tau)u(\tau)d\tau$$

In frequency space, the relation is

$$S(\omega) = R(\omega)U(\omega)$$

where S, R, and U are the Fourier transform of s, r, and u, respectively. The uncorrupted signal can be recovered by finding the optimal filter $\phi(t)$ or its Fourier counterpart $\Phi(\omega)$ which when applied to the measured signal $c(t)$ or $C(\omega)$, and then deconvolved by $r(t)$ or $R(\omega)$, produces a signal that approximate the uncorrupted signal $u(t)$ or $U(\omega)$ with

$$U(\omega) = \frac{C(\omega)\Phi(\omega)}{R(\omega)}$$

In general the optimal filter is defined as

$$\Phi(\omega) = \frac{|S(\omega)|^2}{|S(\omega)|^2 + |N(\omega)|^2}$$

In a preferred embodiment, a kalman filter is used, which is a recursive-estimation filtering technique that tracks the current value of a changing signal.

In a preferred embodiment, the non-linear harmonic response is increased by inducing an asymmetrical response. In a preferred embodiment, this is done by using a system that has a non-reversible redox couple. For example, ferrocene is a redox couple that is very reversible. Thus, the ferrocenes subtended by the ac voltage at a given point, get oxidized on the upswing of the ac voltage and reduced on the down swing. However, If a semi-reversible or non-reversible redox couple is used, for example, the molecule will get oxidized on the up swing and not reduced (or a portion) on the downswing; or vice versa. This will produce even greater non-linearities at certain frequencies.

Three examples of ways to perform this are: use an ETM molecule that gets degraded in the oxidized form, like luminol, use co-reduction or redox mediation, and use enzyme coupled mediation.

In a preferred embodiment, a degradable ETM is used. Basically, the idea is as follows: if some small percentage of the ETM used in the system degrades at every cycle, the signal due to the ETM will degrade over time, while the background signals will not; signals that change over time are generally easily detectable against the background noise. An example is luminol; it will get oxidized on the

upswing, then some of the molecule will undergo a chemical reaction (that is catalyzed by H_2O_2) and be converted to a new molecule. The molecules that are converted before the downswing in the ac voltage will no longer contribute to the ac current. Careful control of the ac frequency and amplitude can adjust the number of molecules that behave in this manner. There are many other examples of molecules that do not undergo reversible redox behavior that could be used in the systems of the invention. The guanines in the DNA themselves are one example.

In a preferred embodiment, non-linearity is achieved through the use of co-reductant or co-oxidant systems. Accordingly, a co-reductant or co-oxidant (collectively, co-redoxant) is used, as an additional electron source or sink. See generally Sato et al., Bull. Chem. Soc. Jpn 66:1032 (1993); Uosaki et al., Electrochimica Acta 36:1799 (1991); and Alleman et al., J. Phys. Chem 100:17050 (1996); all of which are incorporated by reference.

In a preferred embodiment, an input electron source in solution is used in the initiation of electron transfer, preferably when initiation and detection are being done using DC current or at AC frequencies where diffusion is not limiting. In general, as will be appreciated by those in the art, preferred embodiments utilize monolayers that contain a minimum of "holes", such that short-circuiting of the system is avoided. This may be done in several general ways. In a preferred embodiment, an input electron source is used that has a lower or similar redox potential than the ETM of the label probe. Thus, at voltages above the redox potential of the input electron source, both the ETM and the input electron source are oxidized and can thus donate electrons; the ETM donates an electron to the electrode and the input source donates to the ETM. For example, ferrocene, as a ETM attached to the compositions of the invention as described in the examples, has a redox potential of roughly 200 mV in aqueous solution (which can change significantly depending on what the ferrocene is bound to, the manner of the linkage and the presence of any substitution groups). Ferrocyanide, an electron source, has a redox potential of roughly 200 mV as well (in aqueous solution). Accordingly, at or above voltages of roughly 200 mV, ferrocene is converted to ferricenium, which then transfers an electron to the electrode. Now the ferricyanide can be oxidized to transfer an electron to the ETM. In this way, the electron source (or co-reductant) serves to amplify the signal generated in the system, as the electron source molecules rapidly and repeatedly donate electrons to the ETM attached to the nucleic acid. The rate of electron donation or acceptance will be limited by the rate of diffusion of the co-reductant, the electron transfer between the co-reductant and the ETM, which in turn is affected by the concentration and size, etc.

Alternatively, input electron sources that have lower redox potentials than the ETM are used. At voltages less than the redox potential of the ETM, but higher than the redox potential of the electron source, the input source such as ferrocyanide is unable to be oxidized and thus is unable to donate an

electron to the ETM; i.e. no electron transfer occurs. Once ferrocene is oxidized, then there is a pathway for electron transfer.

In an alternate preferred embodiment, an input electron source is used that has a higher redox potential than the ETM of the label probe. For example, luminol, an electron source, has a redox potential of roughly 720 mV. At voltages higher than the redox potential of the ETM, but lower than the redox potential of the electron source, i.e. 200 - 720 mV, the ferrocene is oxidized, and transfers a single electron to the electrode via the conductive oligomer. However, the ETM is unable to accept any electrons from the luminol electron source, since the voltages are less than the redox potential of the luminol. However, at or above the redox potential of luminol, the luminol then transfers an electron to the ETM, allowing rapid and repeated electron transfer. In this way, the electron source (or co-reductant) serves to amplify the signal generated in the system, as the electron source molecules rapidly and repeatedly donate electrons to the ETM of the label probe.

Luminol has the added benefit of becoming a chemiluminescent species upon oxidation (see Jirka et al., *Analytica Chimica Acta* 284:345 (1993)), thus allowing photo-detection of electron transfer from the ETM to the electrode. Thus, as long as the luminol is unable to contact the electrode directly, i.e. in the presence of the SAM such that there is no efficient electron transfer pathway to the electrode, luminol can only be oxidized by transferring an electron to the ETM on the label probe. When the ETM is not present, i.e. when the target sequence is not hybridized to the composition of the invention, luminol is not significantly oxidized, resulting in a low photon emission and thus a low (if any) signal from the luminol. In the presence of the target, a much larger signal is generated. Thus, the measure of luminol oxidation by photon emission is an indirect measurement of the ability of the ETM to donate electrons to the electrode. Furthermore, since photon detection is generally more sensitive than electronic detection, the sensitivity of the system may be increased. Initial results suggest that luminescence may depend on hydrogen peroxide concentration, pH, and luminol concentration, the latter of which appears to be non-linear.

Suitable electron source molecules are well known in the art, and include, but are not limited to, ferricyanide, and luminol.

Alternatively, output electron acceptors or sinks could be used, i.e. the above reactions could be run in reverse, with the ETM such as a metallocene receiving an electron from the electrode, converting it to the metalicenium, with the output electron acceptor then accepting the electron rapidly and repeatedly. In this embodiment, cobalticenium is the preferred ETM.

In this embodiment, non-linearity is achieved because the co-reductant contributes to the current, but only the oxidation current, not the reductive side (or vice versa for co-oxidants).

In a preferred embodiment, non-linearity is achieved through the use of enzyme coupled reactions, such as the glucose peroxidase biosensors. These sensors should have similar behavior as our co-reduction sensors. However, observing the non-linearity in the response should be advantageous.

It appears that in preferred systems, the odd harmonics seem to give a double peak all of the time. The even harmonics always give 1 peak. Also, the even peaks are about 10x larger than the odd. Recall, for a reversible couple, the 3 of peaks is the number of the harmonic, 2 for 2, 3 for 3, etc.

In a preferred embodiment, electron transfer is initiated using alternating current (AC) methods. In addition, the use of AC techniques allows the significant reduction of background signals at any single frequency due to entities other than the ETMs, i.e. "locking out" or "filtering" unwanted signals. That is, the frequency response of a charge carrier or redox active molecule in solution will be limited by its diffusion coefficient and charge transfer coefficient. Accordingly, at high frequencies, a charge carrier may not diffuse rapidly enough to transfer its charge to the electrode, and/or the charge transfer kinetics may not be fast enough. This is particularly significant in embodiments that do not have good monolayers, i.e. have partial or insufficient monolayers, i.e. where the solvent is accessible to the electrode. As outlined above, in DC techniques, the presence of "holes" where the electrode is accessible to the solvent can result in solvent charge carriers "short circuiting" the system, i.e. the reach the electrode and generate background signal. However, using the present AC techniques, one or more frequencies can be chosen that prevent a frequency response of one or more charge carriers in solution, whether or not a monolayer is present. This is particularly significant since many biological fluids such as blood contain significant amounts of redox active molecules which can interfere with amperometric detection methods.

In a preferred embodiment, measurements of the system are taken at at least two separate frequencies, with measurements at a plurality of frequencies being preferred. A plurality of frequencies includes a scan. For example, measuring the output signal, e.g., the AC current, at a low input frequency such as 1 - 20 Hz, and comparing the response to the output signal at high frequency such as 10 - 100 kHz will show a frequency response difference between the presence and absence of the ETM. In a preferred embodiment, the frequency response is determined at at least two, preferably at least about five, and more preferably at least about ten frequencies.

After transmitting the input signal to initiate electron transfer, an output signal is received or detected. The presence and magnitude of the output signal will depend on a number of factors, including the

overpotential/amplitude of the input signal; the frequency of the input AC signal; the composition of the intervening medium; the DC offset; the environment of the system; the nature of the ETM; the solvent; and the type and concentration of salt. At a given input signal, the presence and magnitude of the output signal will depend in general on the presence or absence of the ETM, the placement and distance of the ETM from the surface of the monolayer and the character of the input signal. In some embodiments, it may be possible to distinguish between non-specific binding of label probes and the formation of target specific assay complexes containing label probes, on the basis of impedance.

In a preferred embodiment, the output signal comprises an AC current. As outlined above, the magnitude of the output current will depend on a number of parameters. By varying these parameters, the system may be optimized in a number of ways.

In general, AC currents generated in the present invention range from about 1 femptoamp to about 1 milliamp, with currents from about 50 femptoamps to about 100 microamps being preferred, and from about 1 picoamp to about 1 microamp being especially preferred.

In a preferred embodiment, the output signal is phase shifted in the AC component relative to the input signal. Without being bound by theory, it appears that the systems of the present invention may be sufficiently uniform to allow phase-shifting based detection. That is, the complex biomolecules of the invention through which electron transfer occurs react to the AC input in a homogeneous manner, similar to standard electronic components, such that a phase shift can be determined. This may serve as the basis of detection between the presence and absence of the ETM, and/or differences between the presence of target-specific assay complexes comprising label probes and non-specific binding of the label probes to the system components.

The output signal is characteristic of the presence of the ETM; that is, the output signal is characteristic of the presence of the target-specific assay complex comprising label probes and ETMs. In a preferred embodiment, the basis of the detection is a difference in the faradaic impedance of the system as a result of the formation of the assay complex. Faradaic impedance is the impedance of the system between the electrode and the ETM. Faradaic impedance is quite different from the bulk or dielectric impedance, which is the impedance of the bulk solution between the electrodes. Many factors may change the faradaic impedance which may not effect the bulk impedance, and vice versa. Thus, the assay complexes comprising the nucleic acids in this system have a certain faradaic impedance, that will depend on the distance between the ETM and the electrode, their electronic properties, and the composition of the intervening medium, among other things. Of importance in the methods of the invention is that the faradaic impedance between the ETM and the electrode is

significantly different depending on whether the label probes containing the ETMs are specifically or non-specifically bound to the electrode.

Accordingly, the present invention further provides electronic devices or apparatus for the detection of analytes using the compositions of the invention. The apparatus includes a test chamber for receiving a sample solution which has at least a first measuring or sample electrode, and a second measuring or counter electrode. Three electrode systems are also useful. The first and second measuring electrodes are in contact with a test sample receiving region, such that in the presence of a liquid test sample, the two electrophoresis electrodes may be in electrical contact.

In a preferred embodiment, the apparatus also includes detection electrodes comprising a single stranded nucleic acid capture probe covalently attached via an attachment linker, and a monolayer comprising conductive oligomers, such as are described herein.

The apparatus further comprises an AC voltage source electrically connected to the test chamber; that is, to the measuring electrodes. Preferably, the AC voltage source is capable of delivering DC offset voltage as well.

In a preferred embodiment, the apparatus further comprises a processor capable of comparing the input signal and the output signal. The processor is coupled to the electrodes and configured to receive an output signal, and thus detect the presence of the target nucleic acid.

Thus, the compositions of the present invention may be used in a variety of research, clinical, quality control, or field testing settings.

In a preferred embodiment, the probes are used in genetic diagnosis. For example, probes can be made using the techniques disclosed herein to detect target sequences such as the gene for nonpolyposis colon cancer, the BRCA1 breast cancer gene, P53, which is a gene associated with a variety of cancers, the Apo E4 gene that indicates a greater risk of Alzheimer's disease, allowing for easy presymptomatic screening of patients, mutations in the cystic fibrosis gene, or any of the others well known in the art.

In an additional embodiment, viral and bacterial detection is done using the complexes of the invention. In this embodiment, probes are designed to detect target sequences from a variety of bacteria and viruses. For example, current blood-screening techniques rely on the detection of anti-HIV antibodies. The methods disclosed herein allow for direct screening of clinical samples to detect HIV nucleic acid sequences, particularly highly conserved HIV sequences. In addition, this allows

direct monitoring of circulating virus within a patient as an improved method of assessing the efficacy of anti-viral therapies. Similarly, viruses associated with leukemia, HTLV-I and HTLV-II, may be detected in this way. Bacterial infections such as tuberculosis, chlamydia and other sexually transmitted diseases, may also be detected.

In a preferred embodiment, the nucleic acids of the invention find use as probes for toxic bacteria in the screening of water and food samples. For example, samples may be treated to lyse the bacteria to release its nucleic acid, and then probes designed to recognize bacterial strains, including, but not limited to, such pathogenic strains as, *Salmonella*, *Campylobacter*, *Vibrio cholerae*, *Leishmania*, enterotoxigenic strains of *E. coli*, and Legionnaire's disease bacteria. Similarly, bioremediation strategies may be evaluated using the compositions of the invention.

In a further embodiment, the probes are used for forensic "DNA fingerprinting" to match crime-scene DNA against samples taken from victims and suspects.

In an additional embodiment, the probes in an array are used for sequencing by hybridization.

Thus, the present invention provides for extremely specific and sensitive probes, which may, in some embodiments, detect target sequences without removal of unhybridized probe. This will be useful in the generation of automated gene probe assays.

Alternatively, the compositions of the invention are useful to detect successful gene amplification in PCR, thus allowing successful PCR reactions to be an indication of the presence or absence of a target sequence. PCR may be used in this manner in several ways. For example, in one embodiment, the PCR reaction is done as is known in the art, and then added to a composition of the invention comprising the target nucleic acid with a ETM, covalently attached to an electrode via a conductive oligomer with subsequent detection of the target sequence. Alternatively, PCR is done using nucleotides labelled with a ETM, either in the presence of, or with subsequent addition to, an electrode with a conductive oligomer and a target nucleic acid. Binding of the PCR product containing ETMs to the electrode composition will allow detection via electron transfer. Finally, the nucleic acid attached to the electrode via a conductive polymer may be one PCR primer, with addition of a second primer labelled with an ETM. Elongation results in double stranded nucleic acid with a ETM and electrode covalently attached. In this way, the present invention is used for PCR detection of target sequences.

In a preferred embodiment, the arrays are used for mRNA detection. A preferred embodiment utilizes either capture probes or capture extender probes that hybridize close to the 3' polyadenylation tail of

the mRNAs. This allows the use of one species of target binding probe for detection, i.e. the probe contains a poly-T portion that will bind to the poly-A tail of the mRNA target. Generally, the probe will contain a second portion, preferably non-poly-T, that will bind to the detection probe (or other probe). This allows one target-binding probe to be made, and thus decreases the amount of different probe synthesis that is done.

In a preferred embodiment, the use of restriction enzymes and ligation methods allows the creation of "universal" arrays. In this embodiment, monolayers comprising capture probes that comprise restriction endonuclease ends, as is generally depicted in Figure 6. By utilizing complementary portions of nucleic acid, while leaving "sticky ends", an array comprising any number of restriction endonuclease sites is made. Treating a target sample with one or more of these restriction endonucleases allows the targets to bind to the array. This can be done without knowing the sequence of the target. The target sequences can be ligated, as desired, using standard methods such as ligases, and the target sequence detected, using either standard labels or the methods of the invention.

The present invention provides methods which can result in sensitive detection of nucleic acids. In a preferred embodiment, less than about 10×10^6 molecules are detected, with less than about 10×10^5 being preferred, less than 10×10^4 being particularly preferred, less than about 10×10^3 being especially preferred, and less than about 10×10^2 being most preferred. As will be appreciated by those in the art, this assumes a 1:1 correlation between target sequences and reporter molecules; if more than one reporter molecule (i.e. electron transfer moiety) is used for each target sequence, the sensitivity will go up.

While the limits of detection are currently being evaluated, based on the published electron transfer rate through DNA, which is roughly 1×10^6 electrons/sec/duplex for an 8 base pair separation (see Meade et al., Angw. Chem. Eng. Ed., 34:352 (1995)) and high driving forces, AC frequencies of about 100 kHz should be possible. As the preliminary results show, electron transfer through these systems is quite efficient, resulting in nearly 100×10^3 electrons/sec, resulting in potential femptoamp sensitivity for very few molecules.

All references cited herein are incorporated by reference in their entirety.

EXAMPLES

Example 1

General Methods of Making Substrates and Monolayers

SAM formation on Substrates-General Procedure

The self-assembled monolayers were formed on a clean gold surface. The gold surface can be prepared by a variety of different methods: melted or polished gold wire, sputtered or evaporated gold on glass or mica or silicon wafers or some other substrate, electroplated or electroless gold on circuit board material or glass or silicon or some other substrate. Both the vacuum deposited gold samples (evaporated and sputtered) and the solution deposited gold samples (electroless and electroplated) often require the use of an adhesion layer between the substrate and the gold in order to insure good mechanical stability. Chromium, Titanium, Titanium/Tungsten or Tantalum is frequently employed with sputtered and evaporated gold. Electroplated nickel is usually employed with electroplated and electroless gold, however other adhesion materials can be used.

The gold substrate is cleaned prior to monolayer formation. A variety of different procedures have been employed. Cleaning with a chemical solution is the most prevalent. Piranha solution (hydrogen peroxide/sulfuric acid) or aqua regia cleaning (Hydrochloric acid/ Nitric acid) is most prevalent, however electrochemical methods, flame treatment and plasma methods have also been employed.

Following cleaning, the gold substrate is incubated in a deposition solution. The deposition solution consists of a mixture of various thiols in a solvent. A mixture of alkane thiols in an organic solvent like ethanol is the most prevalent procedure, however numerous variations have been developed. Alternative procedures involve gas phase deposition of the alkane thiol, microcontact printing, deposition using neat thiol, deposition from aqueous solvent and two step procedures have been developed. The concentration of the alkane thiol in the deposition solution ranges from molar to submicromolar range with 0.5-2.0 millimolar being the most prevalent. The gold substrate is incubated/placed in contact with the deposition solution for less than a second to days depending on the procedure. The most common time is 1hr to overnight incubation. The incubation is usually performed at room temperature, however temperatures up to 50°C are common.

Mixed monolayers that contain DNA are usually prepared using a two step procedure. The thiolated DNA is deposited during the first deposition step and the mixed monolayer formation is completed during the second step in which a second thiol solution minus DNA is added. The second step frequently involves mild heating to promote monolayer reorganization.

General Procedure for SAM formation-Deposited from Organic Solution

A clean gold surface was placed into a clean vial. A DNA deposition solution in organic solvent was prepared in which the total thiol concentration was between 400 μ M and 1.0 mM. The deposition solution contained thiol modified DNA and thiol diluent molecules. The ratio of DNA to diluent was usually between 10:1 and 1:10 with 1:1 being preferred. The preferred solvents are tetrahydrofuran

(THF), acetonitrile, dimethylformamide (DMF) or mixtures thereof. Sufficient DNA deposition solution is added to the vial so as to completely cover the electrode surface. The gold substrate is allowed to incubate at ambient temperature or slightly above ambient temperature for 5-30 minutes. After the initial incubation, the deposition solution is removed and a solution of diluent molecule only (100 μ M –1.0 mM) in organic solvent is added. The gold substrate is allowed to incubate at room temperature or above room temperature until a complete monolayer is formed (10 minutes-24 hours). The gold sample is removed from the solution, rinsed in clean solvent and used.

General Procedure for SAM formation-deposited from Aqueous Solution

A clean gold surface is placed into a clean vial. A DNA deposition solution in water is prepared in which the total thiol concentration is between 1 μ M and 200 μ M. The aqueous solution frequently has salt present (approximately 1M), however pure water can be used. The deposition solution contains thiol modified DNA and often a thiol diluent molecule. The ratio of DNA to diluent is usually between 10:1 and 1:10 with 1:1 being preferred. The DNA deposition solution is added to the vial in such a volume so as to completely cover the electrode surface. The gold substrate is allowed to incubate at ambient temperature or slightly above ambient temperature for 1-30 minutes with 5 minutes usually being sufficient. After the initial incubation, the deposition solution is removed and a solution of diluent molecule only (10 μ M –1.0 mM) in either water or organic solvent is added. The gold substrate is allowed to incubate at room temperature or above room temperature until a complete monolayer is formed (10 minutes-24 hours). The gold sample is removed from the solution, rinsed in clean solvent and used.

Monolayers on Au Ball Electrodes

Creating Au Ball Electrodes: Use a razor blade to cut 10 cm lengths of gold wire (127 μ m diameter, 99.99% pure; e.g. from Aldrich). Use a 16 gauge needle to pass the wire through a #4 natural rubber septum (of the size to fit over a ½ mL PCR eppendorf tube). (This serves to support the wire and seal the tubes during deposition. See below.) Use a clean-burning flame (methane or propane) to melt one centimeter of the wire and form a sphere attached to the wire terminus. Adjust the wire length such that when sealed in a PCR tube the gold ball would be positioned near the bottom, able to be submerged in 20 μ L of liquid. On the day of use, dip the electrodes in aqua regia (4:3:1 H₂O:HCl:HNO₃) for 20 seconds and then rinse thoroughly with water.

Derivatization: For 5 minutes, heat 20 μ L aliquots of deposition solutions (2:2:1 DNA/H6/M44 at 833 μ M total in DMF) in PCR tubes on a PCR block at 50°C. Then put each electrode into a tube of deposition solution (submerging just the gold ball — as little of the wire “stem” as possible) and remove to room temperature. Incubate for fifteen minutes before transferring the electrodes into PCR tubes with 200 μ L of 400 μ M M44 in DMF (submerging much of the wire stem as well). Let sit in M44

at room temperature for 5 minutes, then put on the PCR block and run HCLONG. Take electrodes out of the M44 solution, dip in 6x SSC, and place in PCR tubes with 20 μ L of hybridization solution. Dip electrodes in 6x SSC prior to ACV measurement.

HCLONG: 65°C 2', -0.3°C/s to 40°C, 40°C 2', +0.3°C/s to 55°C, 55°C 2', -0.3°C/s to 30°C, 30°C 2', +0.3°C/s to 35°C, 35°C 2', -0.3°C/s to 22°C

Manufacture of Circuit Boards

An 18" x 24" x 0.047" panel of FR-4 (General Electric) with a half-ounce copper foil on both sides was drilled according to specifications (Gerber files). The FR-4 panel is plated with electroless copper (500 microinches) to make the specified drill-holes conductive and then panel is plated with an additional 500 microinches of electroplated copper. Following copper plating, the panel is etched according to specifications via cupric chloride etching (acid etching). The etched panel is then plated with 400 microinches of electroplated nickel with brightner followed by 50 microinches of soft gold (99.99% purity). The gold panel is coated with liquid photoimagable solder mask (Probimer 52, Ciba-Geigy Co.) on both sides of the panel. The imaging is done according to specifications. 14 sensor electrodes that are 250 micron in diameter and 2 larger electrodes (500 microns in diameter) are created with insulated leads leading to gold plated contacts at the edge of the board. The solder masked panel is then scored according to specifications to create individual wafers that are 1" x 1". A silver/silver chloride paste is applied to one of the two larger electrodes (ERCON R-414). The panel is then plasma cleaned with an Argon/Oxygen Plasma mixture. Following cleaning, the panel is stored in a foil-lined bag until use.

Monolayer Deposition on Circuit Boards

The circuit boards are removed from the foil-lined bags and immersed in a 10% sulfuric acid solution for 30 seconds. Following the sulfuric acid treatment, the boards are immersed in two Milli-Q water baths for 1 minute each. The boards are then dried under a stream of nitrogen. The boards are placed on a X-Y table in a humidity chamber and a 30 nanoliter drop of DNA deposition solution is placed on each of the 14 electrodes. The DNA deposition solution consists of 33 μ M thiolated DNA, 33 μ M 2-unit phenylacetylene wire (H6), and 16 μ M M44 in 6x SSC (900 mM sodium chloride, 90 mM sodium Citrate, pH 7) w/ 1% Triethylamine. The drop is incubated at room temperature for 5 minutes and then the drop is removed by rinsing in a Milli-Q water bath. The boards are immersed in a 45°C bath of M44 in acetonitrile. After 30 minutes, the boards are removed and immersed in an acetonitrile bath for 30 seconds followed by a milli-Q water bath for 30 seconds. The boards are dried under a stream of nitrogen.

Example 2

Detection of Target Sequences

Monolayer Deposition on Circuit Boards

As above, the circuit boards were removed from the foil-lined bags and immersed in a 10% sulfuric acid solution for 30 seconds. Following the sulfuric acid treatment, the boards were immersed in two Milli-Q water baths for 1 minute each. The boards were then dried under a stream of nitrogen. The boards were placed on a X-Y table in a humidity chamber and a 30 nanoliter drop of DNA deposition solution was placed on each of the 14 electrodes. The DNA deposition solution consisted of 33 μ M thiolated DNA, 33 μ M 2-unit phenylacetylene wire (H6), and 16 μ M undec-1-en-11yltri(ethylene glycol)(HS-CH₂)₁₁-(OCH₂CH₂)₃-OH) in 6x SSC (900 mM sodium chloride, 90 mM sodium Citrate, pH 7) w/1% Triethylamine. 3 electrodes were spotted with a solution containing DNA 1 (5'-ACCATGGACACAGAT(CH₂)₁₆SH-3'). 4 electrodes were spotted with a solution containing DNA 2 (5'-TCATTGATGGTCTCTTTTAAACA((CH₂)₁₆SH-3'). 4 electrodes were spotted with DNA 3 (5'-CACAGTGGGGGGACATCAAGCAGCCATGCAAA(CH₂)₁₆SH-3'). 3 electrodes were spotted with DNA 4 (5'-TGTGCAGTTGACGTGGAT(CH₂)₁₆SH-3'). The deposition solution was allowed to incubate at room temperature for 5 minutes and then the drop was removed by rinsing in a Milli-Q water bath. The boards were immersed in a 45°C bath of M44 in acetonitrile. After 30 minutes, the boards were removed and immersed in an acetonitrile bath for 30 seconds followed by a milli-Q water bath for 30 seconds. The boards were dried under a stream of nitrogen and stored in foiled-lined bags flushed with nitrogen until use.

Hybridization and Measurement

The modified boards were removed from the foil-lined bags and fitted with an injection molded sample chamber (cartridge). The chamber was adhered to the board using double-sided sticky tape and had a total volume of 250 microliters. A hybridization solution was prepared. The solution contains 10 nM DNA target (5'-TGTGCAGTTGACGTGGATTGTAAAAAGAGACCATCAATGAGGAAGCTGCA GAATGGGATAGAGTCATCCAGT-3' (D-998), 30 nM signaling probe (D-1055) and 10 nM 5'-TCTACAG(N6)C(N6)ATCTGTGTCCATGGT-3' (N6 is shown in Figure 1D of PCTUS99/01705; it comprises a ferrocene connected by a 4 carbon chain to the 2' oxygen of the ribose of a nucleoside). The signalling probe is as follows:

5'-(C23)₄-N87-N87-N87-N87-ATC CAC GTC AAC TGC ACA-3' (D- 1055)

C23	C23	C23	C23
C23	C23	C23	C23
C23	C23	C23	C23
C23	C23	C23	C23

N87 is a branch point comprising a ring structure. C23 is shown in Figure 1F of PCTUS99/01705. In a solution containing 25% Qiagen lysis buffer AL, 455 mM NaClO₄, 195 mM NaCl, 1.0 mM mercaptohexanol and 10% fetal calf serum. 250 microliters of hybrid solution was injected into the

cartridge and allowed to hybridize for 12 hours. After 12 hours, the hybridized chip was plugged into a homemade transconductance amplifier with switching circuitry. The transconductance amplifier was equipped with summing circuitry that combines a DC ramp from the computer DAQ card and an AC sine wave from the lock-in amplifier (SR830 Stanford Instruments). Each electrode was scanned sequentially and the data was saved and manipulated using a homemade program designed using Labview (National Instruments). The chip was scanned at between -100 mV and 500 mV (pseudo Ag/Ag/Cl reference electrode) DC with a 25 mV (50 mV peak to peak), 1000 Hz superimposed sine wave. The output current was fed into the lock-in amplifier and the 1000 Hz signal was recorded (ACV technique). The data for each set of pads was compiled and averaged.

	I_p	Relative Intensity I_p
DNA 1 (Positive 2 Fc)	34 nA	0.11
DNA 2 (Positive Sandwich Assay)	218 nA	0.7
DNA 3 (Negative)	0.3 nA	0.001
DNA 4 (Positive Sandwich Assay)	317 nA	1

Example 3

The use of FFT for signal processing

With the exception a lock-in amplifier, the front-end electronics of the FFT system is essentially the same as the analog instrument. An AC voltage superimposed on top a DC potential ramp is swept through a bio-chip. The chip's output current passes through a transimpedance amplifier where the signal is amplified and converted into volts. At this point, instead of going to a lock-in amplifier, the signal is directly digitized and analyzed. Recently, we have added an analog anti-alias filter before digitization. The anti-alias filter is used to reduce white noise above the frequencies of interest prior to digitization. It is necessary to filter high frequencies before digitization because any post analog-to-digital conversion (ADC) filtering will suffer from alias effects if we do not limit the bandwidth of our signal. The analog anti-alias filter is essentially a high poles or order low-pass filter.

The signal is digitized using a analog to digital converter (e.g. 12-Bit, 1.25 MS/s data acquisition card from National Instrument (NI-DAQ Model PCI-MIO-16E-1). A custom-made Labview-based program was developed to analyze the data. Typically, 1.25×10^6 samples are acquired at 100 kHz for 12.5 seconds with no windowing. These values were chosen based on the following factors: 1) the desire for fast computational time which limits the number of samples we want to analyze and 2) minimizing alias effects. Hence we opt for 1.25×10^6 samples per run and $f_{\text{sampling}} = 100 \text{ kHz}$). Recall that the sampling rate determines how often an analog-to-digital conversion (ADC) takes place. A fast sampling rate acquires more points in a sampling period and can therefore, form a better

representation of the original signal than a slow sampling rate. Sampling too slowly may result in a poor representation of the analog signal. The effect of under sampling is that the signal appears as if it has a different frequency than it truly does. This misrepresentation of a signal is called an alias. The use of a lowpass filters and high sampling rate minimize alias in our data.

RESULTS

Buffer solution versus complementary DNA

The sinusoidal AC Voltammetry technique involves adding a sine wave, typically 10-1000 Hz, on top of the DC ramp. All of the data shown in this report were taken at 1 kHz. Recall that the frequency spectrum of a sinusoidal at a fixed frequency is simply a single peak at that frequency with the height of the peak being the amplitude of the wave. For instance, a 1000 Hz sine wave with 10 V_{rms} will show up as a 10 V_{rms} peak at 1000 Hz in the frequency domain. However, since the bio-chip is a non-linear device, a harmonic distortion of the sinusoidal will occur and the chip response will contain harmonics.

Figure 4A is the frequency spectrum of a bio-chip with only buffer solution (700 mM NaClO₄:300 mM NaCl). The 1000 Hz peak is the dominant peak in the spectrum. There are also harmonics of the 1 kHz but they drop off quickly. In fact, the difference between the fundamental frequency and the second harmonic is almost 2 orders of magnitude! This suggests a rather weak harmonic distortion, weak, but measurable. The amplitude of the harmonics (excluding the fundamental frequency) drops off exponentially. In this case, the exponential decay has a slope of $k \approx -2.15$ on the log scale (we will refer to the value k as the harmonic decay value in the rest of the report).

Figure 4B is the frequency spectrum of a bio-chip after hybridization with 1 μ M complementary DNA. The same chip from the buffer solution measurement was used in this measurement for control purposes. Since the same chip was used, the background signature of the two measurements is essentially the same. An obvious difference between Fig. 4b and Fig. 4a is the amplitude of the harmonic peaks, particularly high harmonics. This suggests that the harmonic distortion is stronger in the presence of a redox chemical system with a significant faradaic impedance component. Figure 6 highlights two key differences between the two measurements: signal size and shape. Above, a harmonic decay value of $k \approx -2.15$ was reported for the buffer solution measurement. In the case of the 1 μ M complementary DNA measurement, $k \approx -0.83$, indicating the high harmonic signal is quite large. Another distinctive feature of the complementary DNA measurement is the structure of the harmonic peaks. Figure 7 illustrates this result. We observe that in the presence of a Nernst distribution of electrons, there are multiple-peak structures, typically in pairs, in the harmonic peaks. The multiple peak structure is observed at all high n ($n \geq 2$) harmonic numbers in all samples with bound molecules. Note that the peak of the signal is not at the harmonic frequency but at $v_n \pm \Delta v$.

Detection levels

In Figure 7, the peak amplitudes of the FFT spectra are plotted at different frequencies for a 1 μ M, 100 nM, 10 nM, and 1 nM DNA measurements. We also included data from the buffer solution measurement for comparison and benchmarking. Several obvious conclusions can be made from Fig. 7. The first is the peak amplitude. As expected, the higher concentration measurements yield larger signals. Surprisingly, however, the amplitude does not scale linearly with the concentration (i.e. the signal from 1 μ M is not 10 \times the 100 nM value). Perhaps this is due to not knowing the exact $T_{1/2}$ for each concentration. Data from Figure 6 suggest that we either measured the 1 μ M concentration too early ($t < T_{1/2}$ of 1 μ M) or measured the 100 nM too late ($t > T_{1/2}$ of 100 nM). A common trend in measurements is the slope of the harmonic peak ($n \geq 2$), which is an indication of the strength of the harmonic distortion and/or the non-linearity of the system. The flatter the slope, the larger the high harmonic peaks and thus, the system is more non-linear. In the case of the 1 μ M, 100 nM, and 10 nM, where we have good signals, the slopes are relatively the same with $k \approx -1$. We do see the slope becoming steeper as the concentration decreases and signal to noise (S/N) degrades. Another commonality of the 1 μ M, 100 nM, and 10 nM DNA signal is the familiar structure of the harmonic peaks (i.e. splitting of the peak, see Figure 6). Measurement at 1 nM did not yield good data. We did not see structure in any of the harmonic peaks and the slope of the harmonics is much steeper in comparison to the higher concentration measurements. In fact, the slope of the 1 nM harmonic signal is closer to $k = -2$, approximately the same level as the buffer solution measurement.

Example 4

The use of JTFT

Similar to FFT, the raw data $i(t)$ is archived and digitally processed. Since the unprocessed data is archived, more thorough analysis can be done in the post-processing step at the experimentalist's leisure. The system can be used to produce a frequency spectrum quickly after a scan (within a few minutes) for immediate data analysis. Alternatively, with the use of JTFT algorithms (Signal Processing Toolset, National Instrumentation Corp.) the data can be post-processed to produce a full spectrogram where the spectrogram gives time waveforms (or current versus DC potential waveforms) similar to that obtained by the analog machine, but for all harmonics in a single scan. Accordingly, the time-dependent frequency spectrum can reveal patterns in the signal that would otherwise unobservable in either time waveforms or time-independent spectrum. Another advantage provided by JTFT is the detection of noise-corrupted signal. Since random or white noise typically have no time nor frequency dependent while signals are usually concentrated in time and frequency space, the signal to noise ratio will increase if one uses JTFT.

Joint Time-Frequency Transform

The fastest and simplest approach for calculating a joint-time frequency spectrogram is Short Time Fourier Transform whereby the time-dependent signal is divided into overlapping time bins (see Qian et al., Joint time frequency analysis; Englewood Cliffs, N.J. Prentice Hall 1996; Wexler et al, Signal Processing 21.3:207 (1990); Qian et al., Signal Processing 25.2125 (1992); Cohen et al., J. Math. Phys. 7:781 (1966); Choi et la., IEEE Trans. Acoustics, Speech, Signal Processing 37.6:862 (1989); and Zhao et al., IEEE Trans. Acoustics, Speech, Signal Processing 38.7:1084 (1990), all of which are expressly incorporated by reference). One can then apply Fourier Transform to each time bin to produce a rough joint time-frequency spectrogram. Other joint time-frequency algorithms include Gabor transform and transforms that use the Wigner-Ville, Pseudo Wigner-Ville, Cohen's class, Choi-Williams, and cone-shape distributions. There are advantages and disadvantages with each algorithm. For example, the STFT spectrogram is fast and robust but suffers from poor resolution and produces non-negative results. The adaptive spectrogram provides extremely high resolution when a signal is made up of linear chirps and does not produce artificial cross terms; however, the algorithm is slower and also does not give negative results.

Figure 8 illustrates a spectrogram from a biochip using a pos-processing routine. The lower graph is a time waveform of the total current produced by the cell. This signal is essentially the raw output from the alternating current voltammetry (ACV) scan. The standard fast Fourier transform (FFT) produced the frequency spectrum on the right. This scan can be done immediately after the data is archived. Typically, a scan will take less than 15 seconds and the FFT takes about 30 seconds and a Pentium II PC. The spectrogram on top is the result of a short time-frequency transform. The current version of Labview does not support three-dimensional plots and thus we are presently limited to just contour plots with Labview. The post processing routine used to produce the spectrogram requires a few minutes (less than 5) depending on the JTFA algorithm.

Figure 9 is a 3-D plot of the spectrogram from an ACV scan. From figure 9, we see the familiar current versus DC potential voltammograms at fundamental (1 kHz) and 4th harmonic (4 kHz) frequencies. In addition, the 2nd and 3rd harmonic voltammograms were obtained in the very same scan. The fact that we can obtain all harmonics in the same scan will allow us to better study our system.

Note behavior of the signal to background from the JTFT data. Figure 10 illustrates ACV voltammograms at the fundamental and first three harmonic frequencies. The data shown in these plots came from the spectrogram of figure 10. Clearly, the background capacitance is largest at the fundamental harmonic. At higher harmonics, capacitance dropped dramatically (more than 2 orders of magnitude). This is consistent with the notion that the double layer and monolayer capacitance are nearly linear and do not produce strong harmonic signal. However, the faradaic component is

nonlinear and does produce strong harmonics. Accordingly, our signal to background ratio increases at higher harmonic numbers.

CLAIMS

We claim:

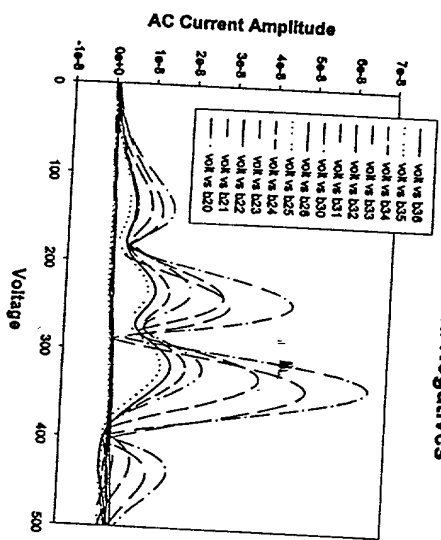
1. A method of detecting target analytes in a sample comprising:
 - a) providing an array comprising a plurality of electrodes, at least one of which comprises an assay complex comprising:
 - i) a capture binding ligand covalently attached to said electrode;
 - ii) a target analyte; and
 - iii) an electron transfer moiety;
 - b) applying a first input signal to said assay complex;
 - c) receiving an output signal;
 - d) processing said output signal to detect the presence of said target analytes.
2. A method according to claim 1 wherein said processing comprises higher harmonic analysis.
3. A method according to claim 1 wherein said processing comprises a fast Fourier transform (FFT) analysis.
4. A method according to claim 1 wherein said processing comprises JTFT.
5. A method according to claim 1 wherein said processing comprises the use of a peak recognition scheme.
6. A method according to claim 1 wherein said processing comprises a digital filter.
7. A method according to claim 1 wherein said processing comprises signal averaging.
8. A method according to claim 1 wherein said processing comprises spectral analysis.
9. A method according to claim 1 wherein said processing comprises peak recognition.
10. A method of detecting target analytes in a sample comprising:
 - a) providing an array comprising a plurality of electrodes, at least one of which comprises an assay complex comprising:
 - i) a capture binding ligand covalently attached to said electrode;
 - ii) a target analyte; and

- iii) an electron transfer moiety;
- b) applying a first input signal to said assay complex, wherein said input signal comprises the sum of multiple frequencies at a plurality of amplitudes;
- c) receiving an output signal;
- d) processing said output signal to detect the presence of said target analytes.

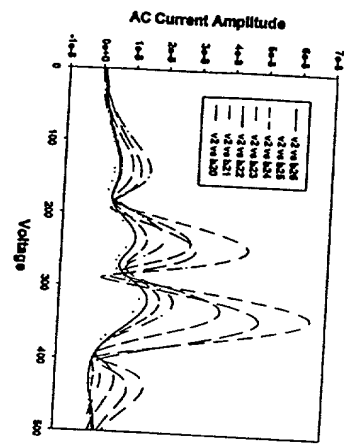
ABSTRACT

The invention relates to the use of signal processing methods in order to achieve higher signal to noise ratios, to increase the detection limits of target analytes. These techniques include the monitoring of the output signal at higher harmonic frequencies.

Positives and Negatives



Positives



Negatives

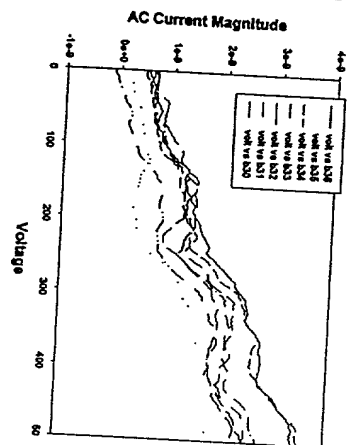


Fig 1

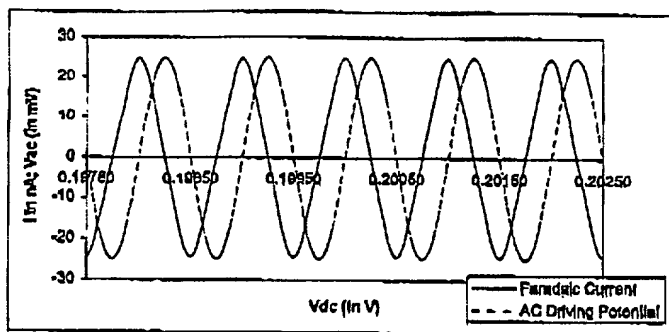
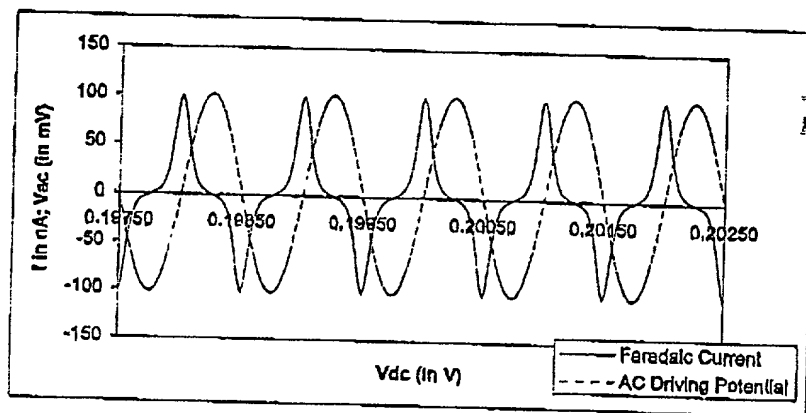
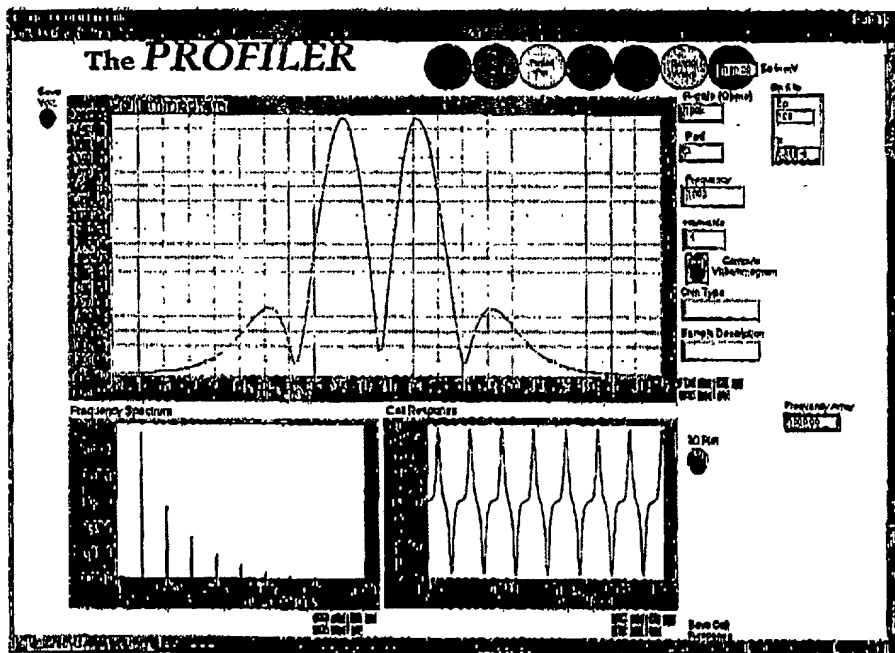


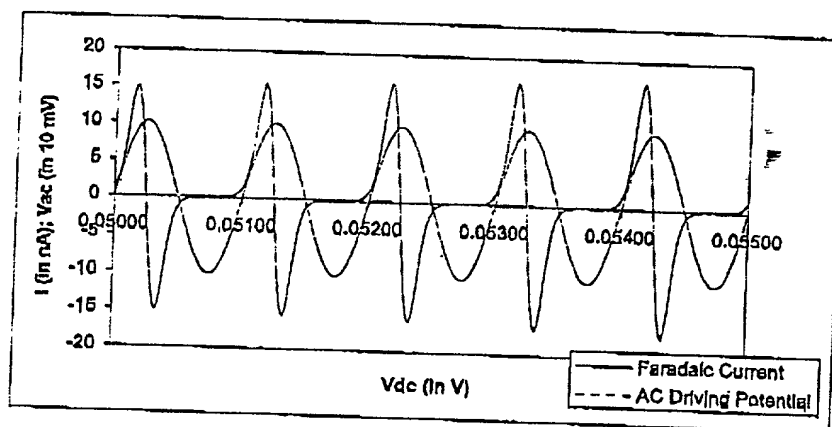
Fig 2A



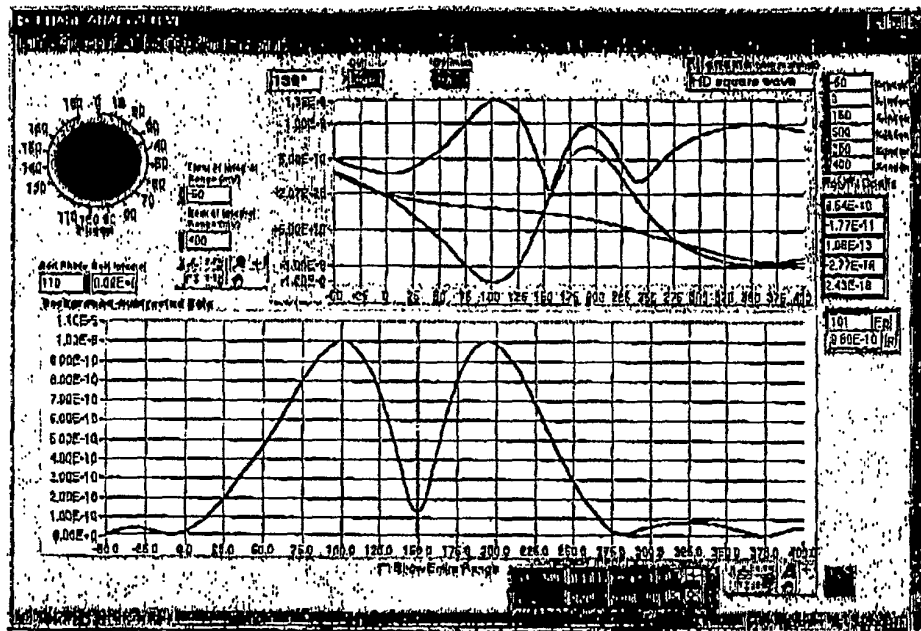
2B



2C



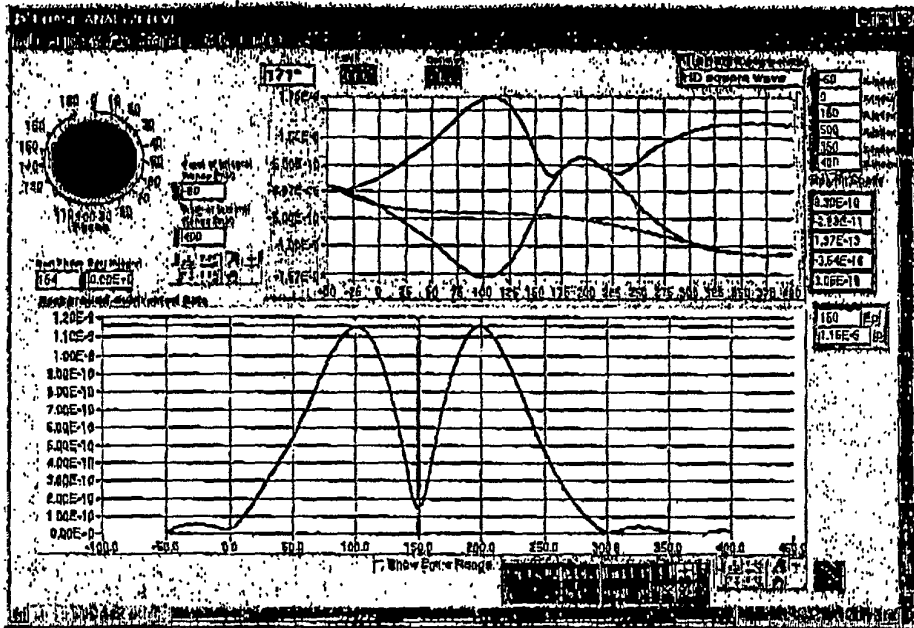
2D



2nd harmonic SW

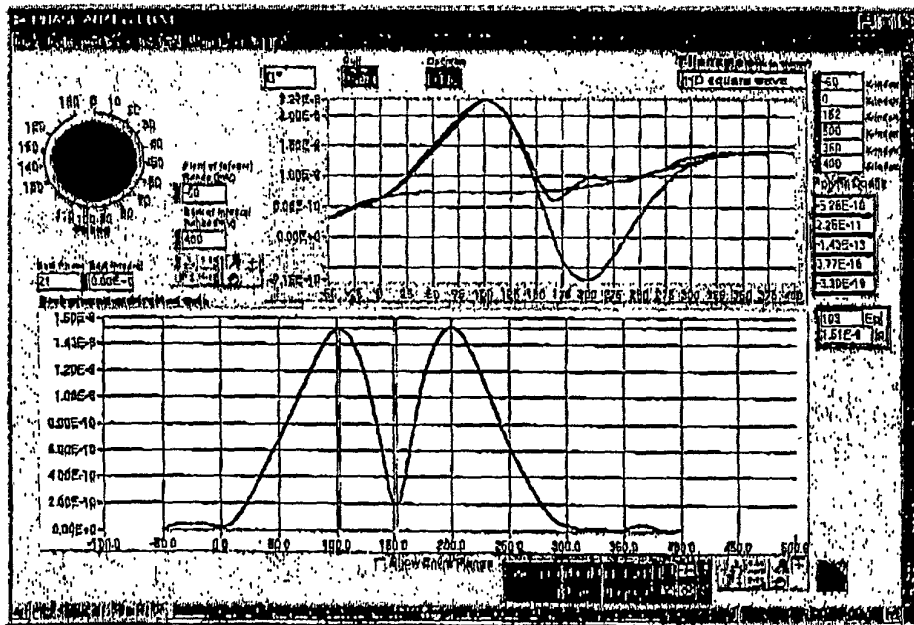
Fig 3A

3B



4th harmonic SW

3C



6th Harmonic SW

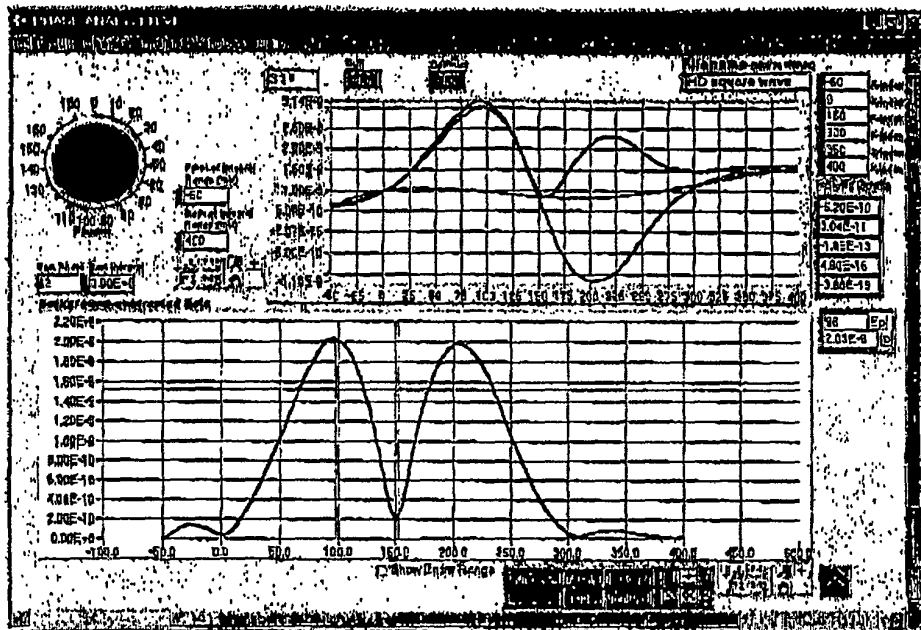
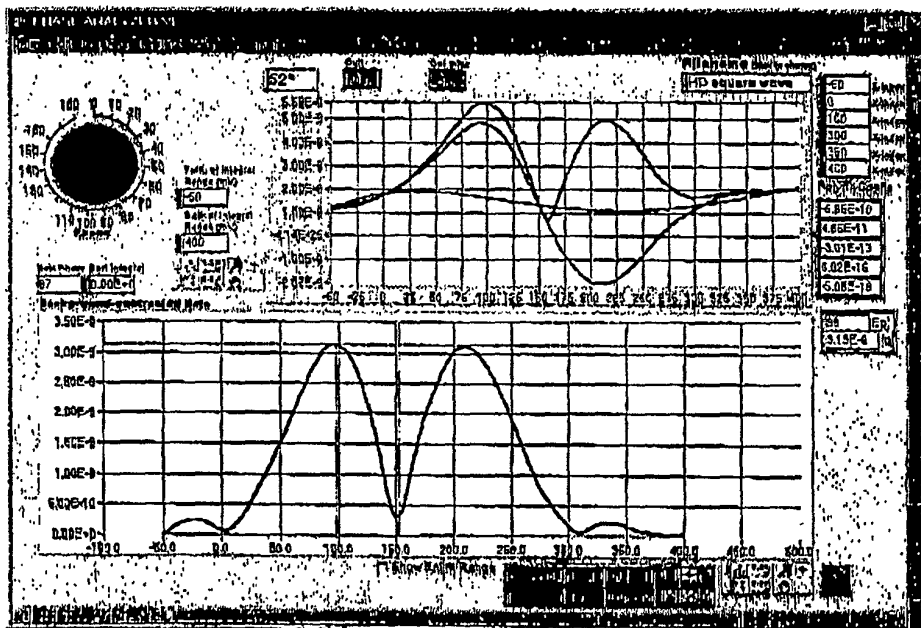


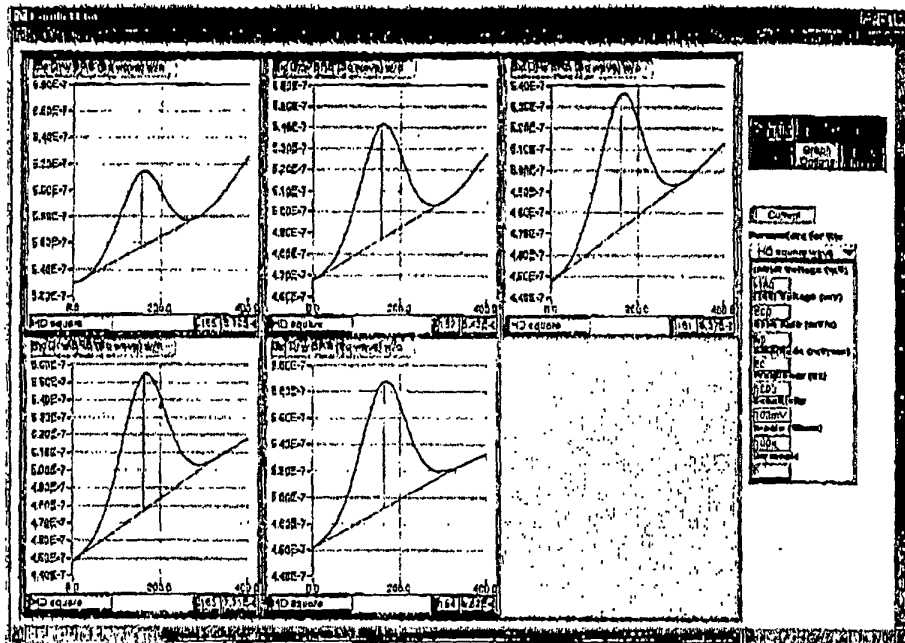
Fig 3D

8th Harmonic SW

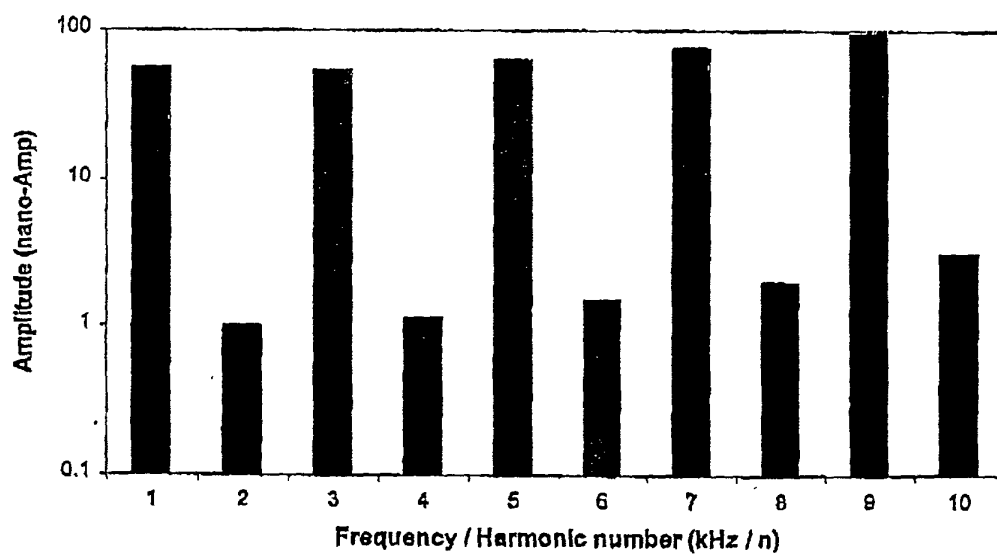


3E

10th harmonic SW



1,3,5,7, and 9th harmonic SW



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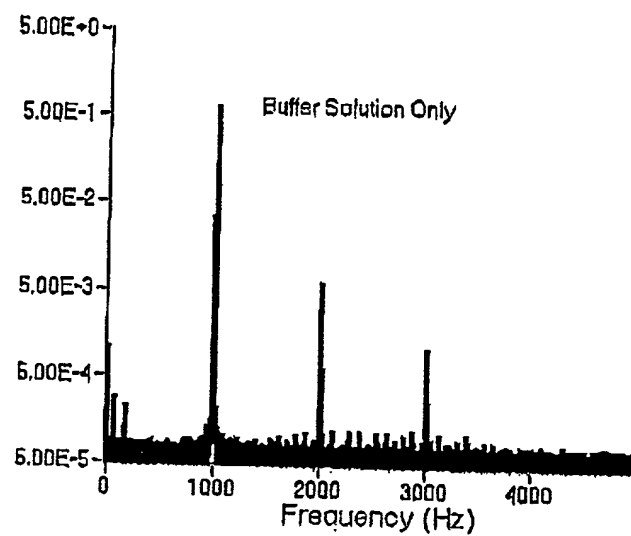


Fig 4A

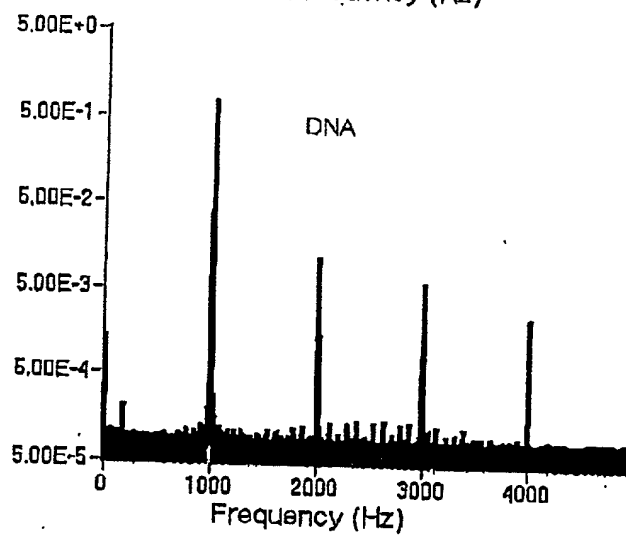
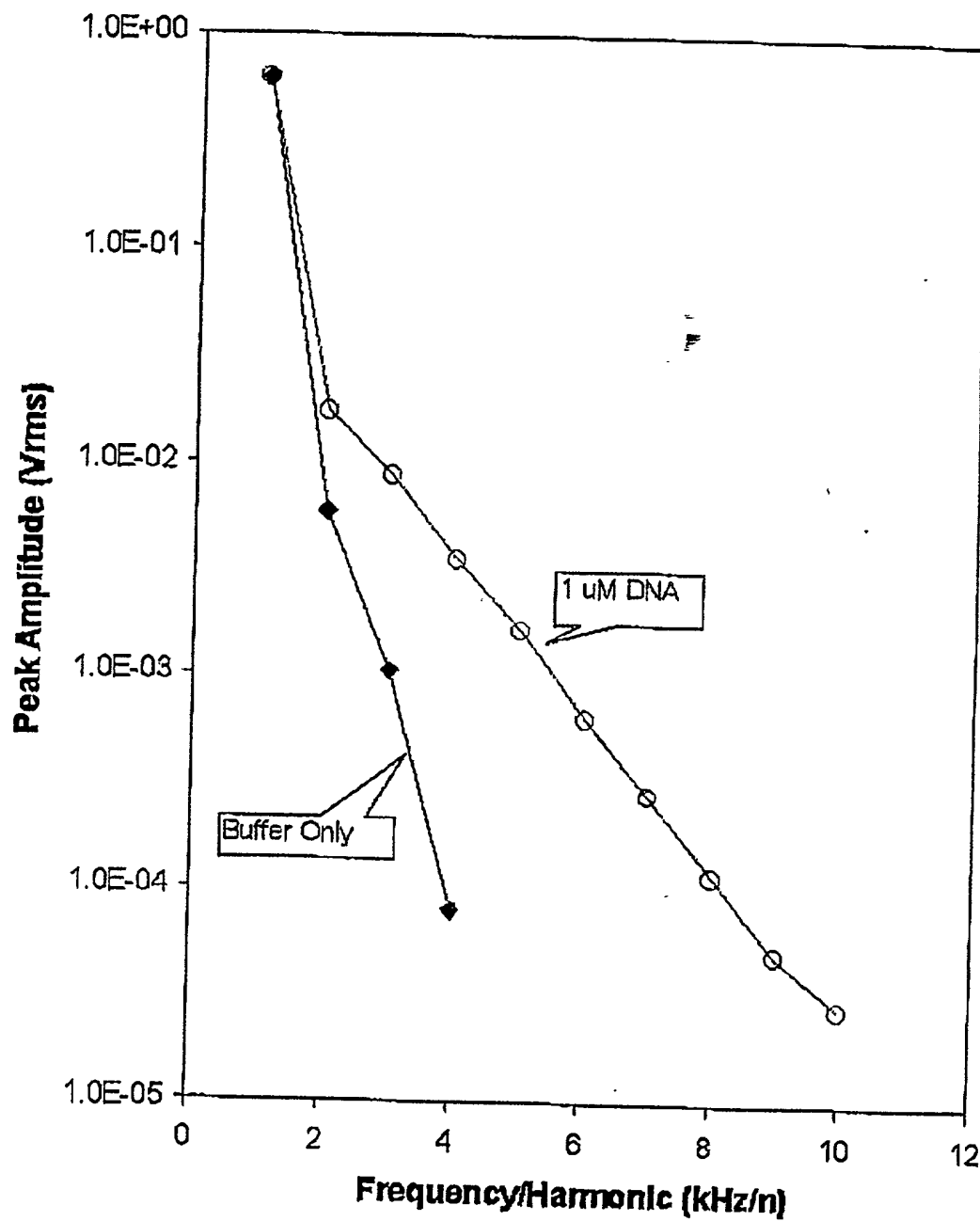


Fig
4B

Fig 5



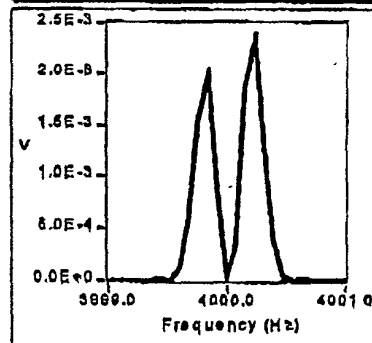
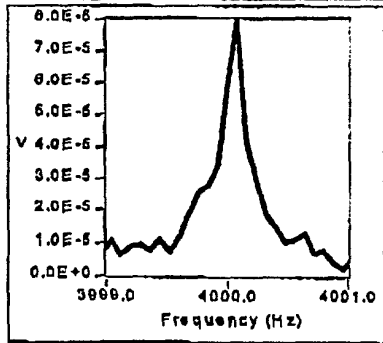
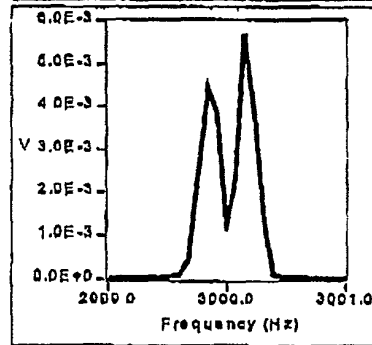
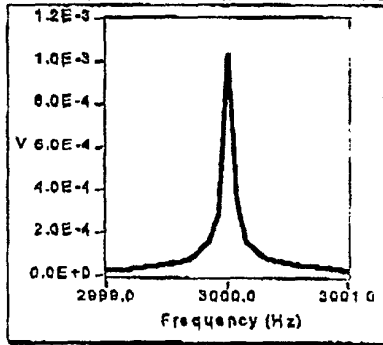
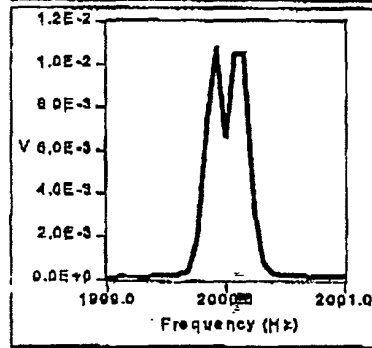
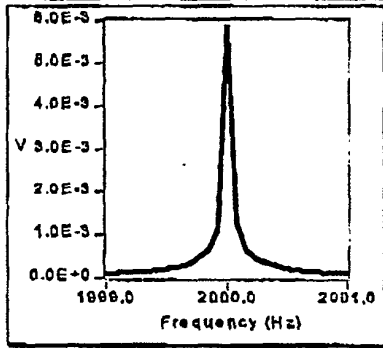
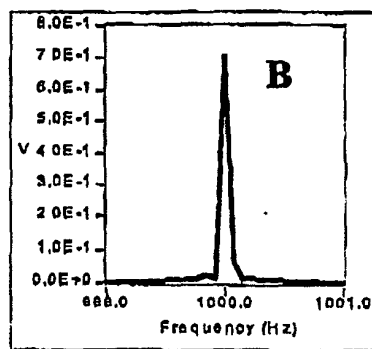
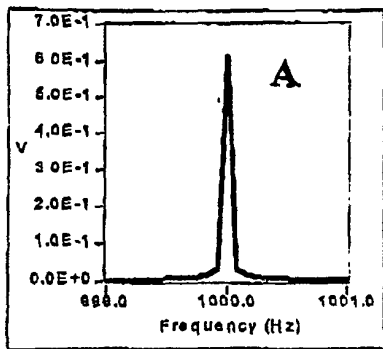


Fig 6

Sinusoidal ACV FFT Spectrum at various DNA Concentrations

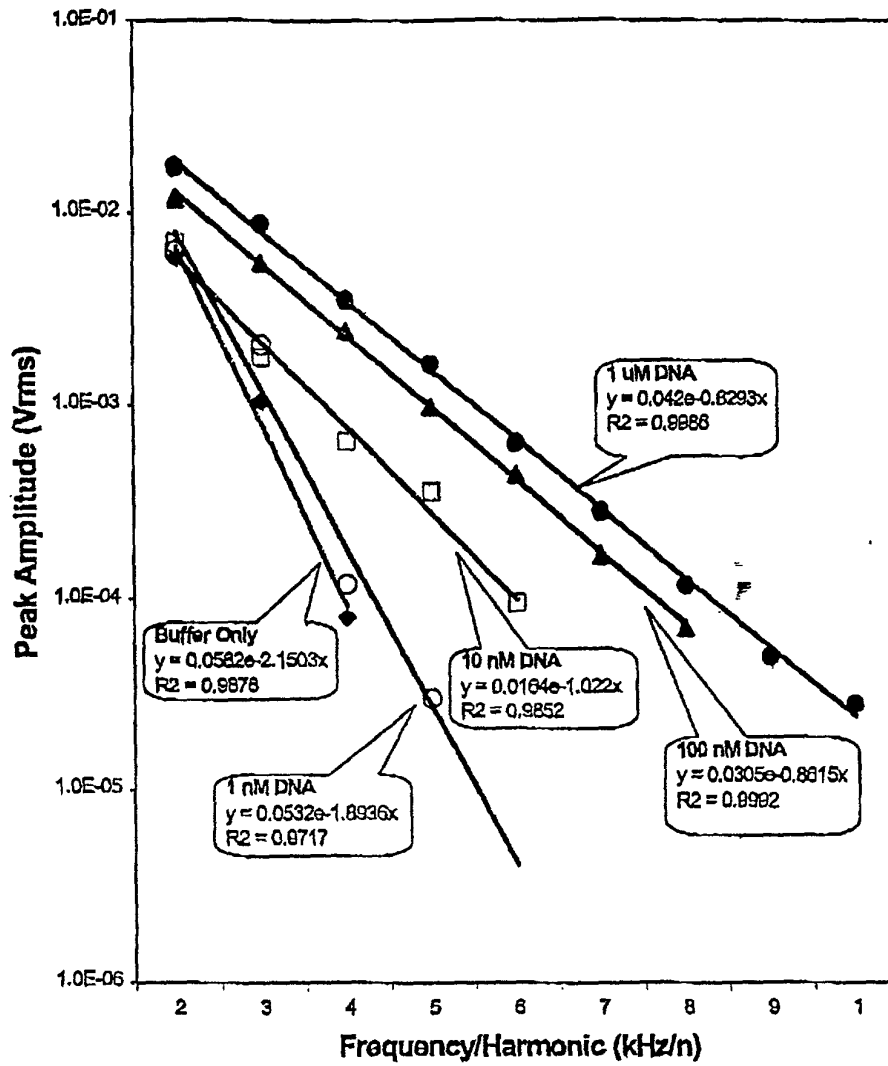


Figure 4. Results from the detection level study. The y-axis is the peak amplitude of the harmonics ($n \geq 2$) at different DNA concentration (1 μ M - 1 nM) and the x-axis is the frequency and harmonic number. Also shown are data from the buffer solution measurement.

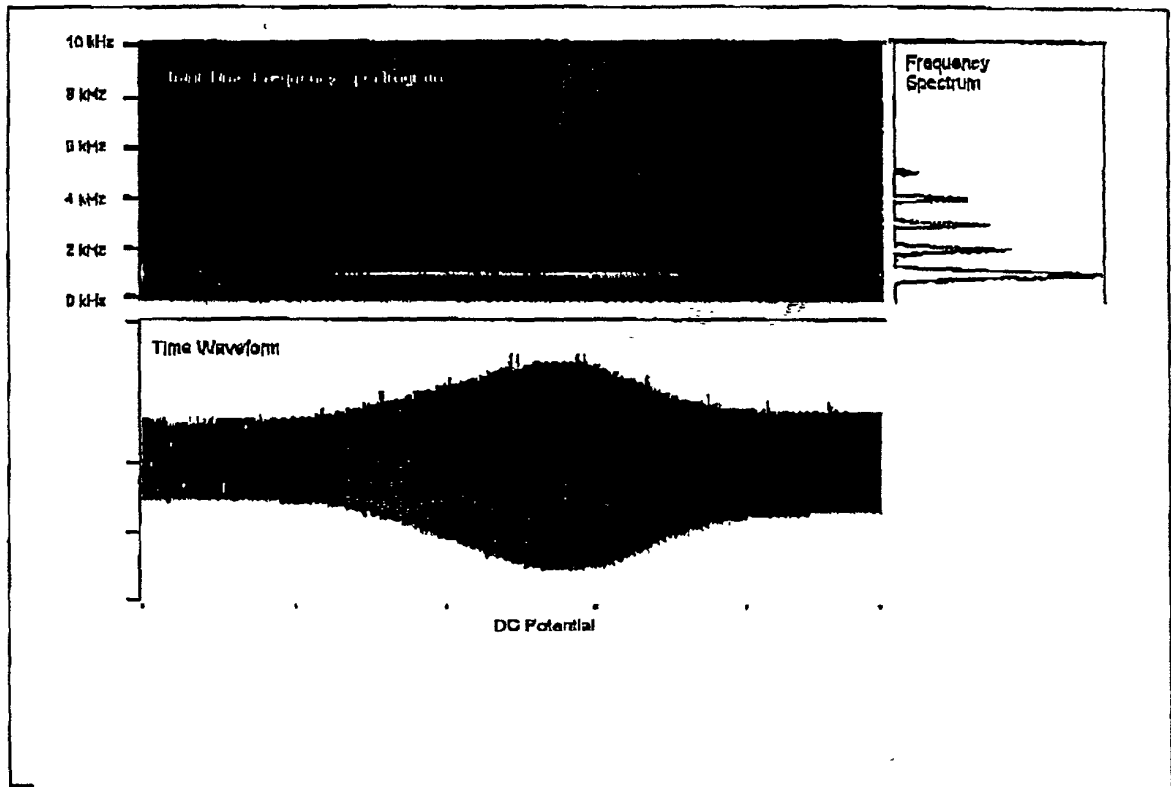


Fig 8

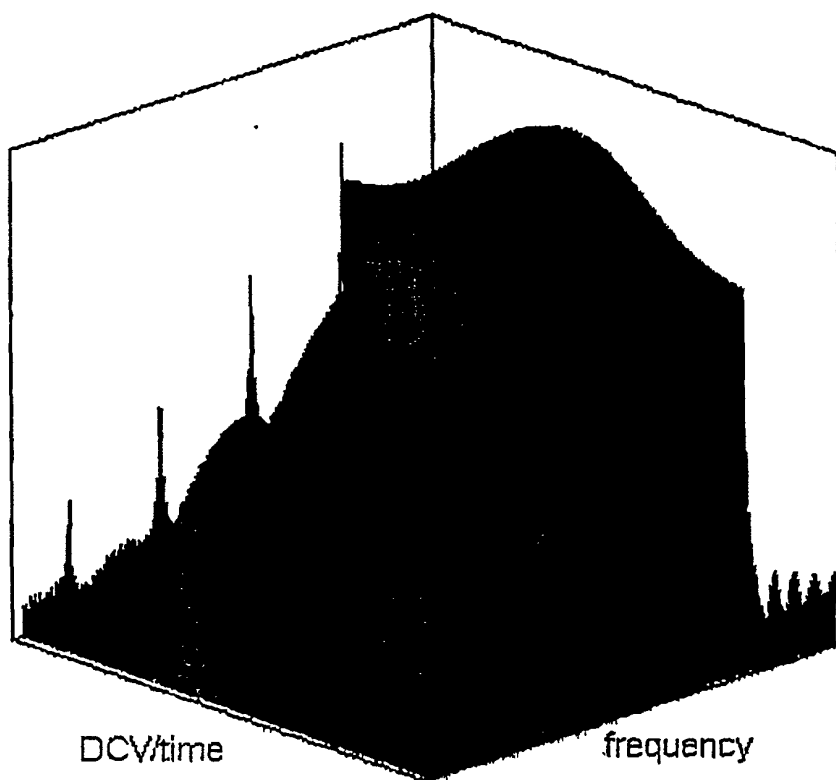


Figure 2. Three-dimensional spectrogram of an ACV scan of a CMS biochip. The amplitude of the cell current is plotted on a log scale to emphasize the higher harmonics. The spectrogram clearly shows the familiar first and fourth harmonic voltammograms. All without a tuned or lock-in ampl. More importantly, other harmonics are also present in the spectrogram.

Fig 9

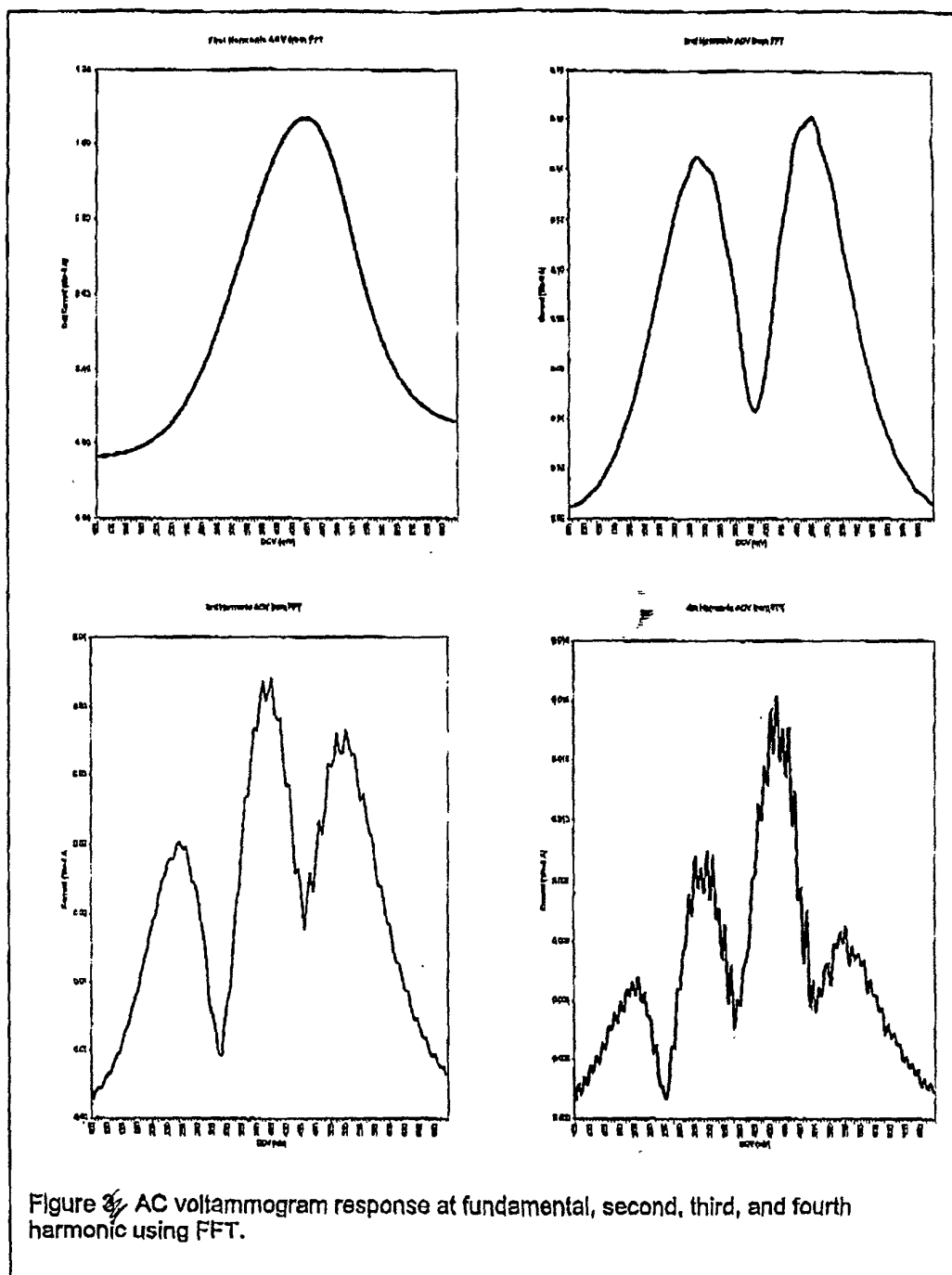


Figure 3. AC voltammogram response at fundamental, second, third, and fourth harmonic using FFT.

Fs 10